



PATENT
Attorney Docket: 53356-5001-US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: **G. Lenzen *et al.***

Application No. **09/319,724**

Filed: **September 8, 1999**

For: **MAMMALIAN ICYP
(IODOCYANOPINDOLOL) RECEPTOR
AND ITS APPLICATIONS**

Group Art Unit: **1646**

Examiner: **Michael T. Brannock**

RECEIVED

JUL 28 2003

Commissioner for Patents
Washington, D.C. 20231

TECH CENTER 1600/2900

DECLARATION UNDER 37 CFR §1.132 BY TOSHINARI SUGASAWA

I, Toshinari Sugasawa, declare as follows:

1. I am a co-inventor of the subject matter described and claimed in the above-referenced patent application, U.S. Patent Application No. 09/319,724. A bibliography of relevant publications and my curriculum vitae are attached hereto.
2. I have read and understand the non-final Office Action (paper no. 16) that was mailed March 24, 2003, in the above-referenced application, including the rejection for lack of enablement under 35 U.S.C. §112, first paragraph. It is my understanding that the basis for the rejection is that the specification, while being enabled for polynucleotides encoding a protein of SEQ ID No. 14 and the portion thereof capable of binding ICYP, allegedly fails to provide sufficient guidance for polypeptides that are not 100% identical to SEQ ID No. 14, *i.e.*, substitutions, deletions and insertions, but which still retain a desired property of the polypeptide of SEQ ID No. 14.
3. The specification reports the identification and cloning of the human ICYP receptor following the identification of a human expressed sequence tag (EST) using the tBLASTn program. The human fragment was identified based on homology with a highly conserved

formic acid cleaved fragment of the rat protein (SEQ ID No. 6), which demonstrated almost 100% homology to the corresponding human sequence identified (SEQ ID No. 5) (see Example 3 starting on page 32).

This suggests that this family of proteins is highly conserved across species, and that the same, well known methodology used to clone the human gene could also be used without undue experimentation to clone natural variants from other species.

4. In line with the methodology reported in Example 3 of the specification, this declaration describes the results of tBLASTn database searches using the fragments represented by SEQ ID Nos. 5 and 6. As shown in the attached tBLASTn results, when conducted with the amino acid sequence of SEQ ID No. 5, the search revealed 14 clones showing 100% homology in the region of the fragment represented by SEQ ID No. 5. Most all of these clones reveal homologous animal ICYP receptors, including the receptor from human, mouse, *C. elegans*, zebra fish, etc. (Note that TM9SF3 (transmembrane protein 9 superfamily member 3) and SMBP (SM-11044 binding protein) and ICYP receptor are the same protein.)

5. When the tBLASTn search was conducted with the amino acid sequence of SEQ ID No. 6, which comprises an "X" in the amino acid sequence of the formic acid cleaved fragment, 16 clones were identified including chicken and fruit fly TM9SF3. Thus, the fragment used in Example 3 of the specification to identify human ICYP receptor cDNA using the tBLASTn program could also be used in the same manner to identify natural variants from other species. Furthermore, clones corresponding to the identified sequences could be readily isolated by one of skill in the art using the methodology outlined in Example 3.

6. I further declare that all statements made herein of my own knowledge are true, and that all statements made on information and belief are believed to be true, and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

By: 蒙米敏成

Dated: 9 July 2003

CURRICULUM VITAE

Name: Toshinari Sugasawa, Ph.D.
Sex: Male
Date of birth: 29 December, 1959
Place of birth: Tokyo, Japan
Marital status: Married
Nationality: Japanese
Present address: Discovery Research Laboratories II, Research Division,
Sumitomo Pharmaceuticals Co., Ltd.
3-1-98, Kasugade Naka 3-Chome, Konohana-ku,
Osaka 554-0022, Japan
Phone: (81)6(6466)5269
Fax: (81)6(6466)5182
Home address: 8-35-607, Wakayama-cho, Nishinomiya-shi,
Hyogo 663-8016, Japan
Phone: (81)798(63)6075
Fax: (81)798(63)6075

Education:

1992-1996 Institut Cochin de Génétique Moléculaire,
Laboratoire d'Immuno-Pharmacologie Moléculaire, CNRS-UPR 0415
and
Unités de Formation et de Recherche - Biochimie,
Université Paris VII

Awarded the Doctor of Science for a thesis entitled "Caractérisation Pharmacologique, Biochimique et Immuno-chimique d'une Nouvelle Protéine Liant l'Iodocyanopindolol: "ICYPBP".

Concentrations: Purification, amino-acid sequencing and cDNA cloning of a novel membrane protein. Transfection of the plasmid DNA into the mammalian host cells. Pharmacological and biochemical analysis of the transfectants.

Professor: Dr. A. Donny Strosberg

1979-1983 Department of Animal Science, Faculty of Agriculture,
Kyoto University

Awarded the Bachelor's Degree, Science in Agriculture for a thesis
entitled "In vitro fertilization of Mongolian Gerbill eggs".

Concentrations: Study of the suitable culture medium composition for
in vitro fertilization of mammalian eggs.

Professor: Dr. Akira Iritani

Research and professional experience:

1983-1992 Research fellow at the Department of Pharmacology, Research
Laboratories, Sumitomo Pharmaceuticals Co., Ltd., working on the
pharmacological studies of phenylethanolamine-derivatives and
anti-asthmatic/allergic agents.

1997-present Senior Research Scientist at the Discovery Research Laboratories II,
Research Division, Sumitomo Pharmaceuticals Co., Ltd., working on
the pharmacological studies of anti-asthmatic/allergic agents.

Publications

- 1) Sugasawa T., Lenzen G., Simon S., Hidaka J., Cahen A., Guillaume J.-L., Camoin L., Strosberg A. D. and Nahmias C., The iodocyanopindolol and SM-11044 binding protein belongs to the TM9SF multispinning membrane protein superfamily., *Gene*. 273: 227-37 (2001)
- 2) Sugasawa T., Matsuzaki-Fujita M., Guillaume J.L., Camoin L., Morooka S. and Strosberg A. D., Characterization of a novel iodocyanopindolol and SM-11044 binding protein, which may mediate relaxation of depolarized rat colon tonus., *Journal of Biological Chemistry*. 272:21244-52 (1997)
- 3) Sugasawa, T. and Morooka S., Existence of Atypical β -Adrenoceptor on Guinea-pig Eosinophil., in Recent Advances in Cellular and Molecular Biology (Wegmann, R.J. and Wegmann, M.A., eds) Vol.3, pp 223-227, Peeters Press, Leuven, Belgium (1992)

- 4) Sugasawa T. and Morooka S., Effect of BRL-35135 on LTB₄-induced guinea pig eosinophil chemotaxis., *Agents & Actions*. 37:232-7 (1992)
- 5) Sugasawa T., Matsuzaki M., Morooka S., Foignant N., Blin N. and Strosberg A. D., In vitro study of a novel atypical beta-adrenoceptor agonist, SM-11044., *European Journal of Pharmacology*. 216:207-15 (1992)
- 6) Sugasawa T., Imanishi N. and Morooka S., Effect of the selective PAF antagonist SM-10661 on an asthmatic model. 2. Effect on antigen-induced dual asthmatic response and infiltration of leukocytes into airways in actively sensitized conscious guinea pigs., *Lipids*. 26:1305-9 (1991)
- 7) Uchida M., Imanishi N., Sugasawa T. and Morooka S., Effect of the selective PAF antagonist SM-10661 on an asthmatic model. 1. Effect on passive anaphylactic bronchoconstriction in guinea pigs., *Lipids*. 26:1301-4 (1991)



translating

BLAST

Nucleotide

Protein

Translations

Retrieve results for an
RID

Search

DPSFFQHRHWFSIFNS

Choose a translation PROTEIN query - TRANSLATED database [tblastn]

Set subsequence From: To:

Choose database nr

Genetic codes Disabled

Now: BLAST or Reset query Reset all

Options for advanced blasting

Limit by entrez query or select from: (none)

Choose filter ☒ Low complexity ☐ Mask for lookup table only ☐ Mask lower case

Expect 10

Word Size 3

Matrix BLOSUM62 Gap Costs Existence: 11 Extension: 1

Other advanced

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment in HTML format

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Limit results by entrez query or select from: (none)

Expect value range:

Layout: Two Windows Formatting options on page with results: None

Autoformat Semi-auto



results of BLAST

TBLASTN 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs". Nucleic Acids Res. 25:3389-3402.

RID: 1054277721-021460-25890

Query=

(17 letters)

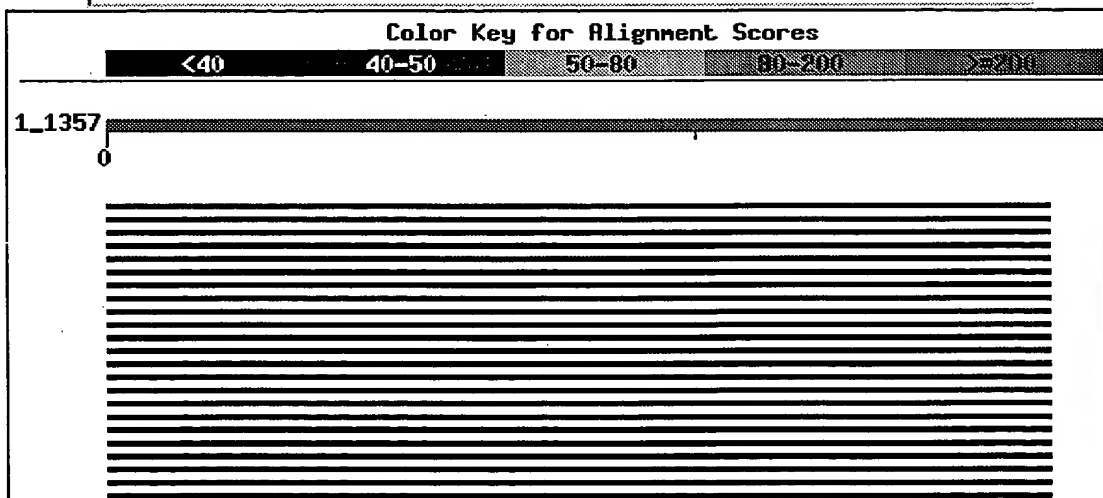
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

1,772,460 sequences: 8,313,506,101 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 23 Blast Hits on the Query Sequence**

Mouse-over to show define and scores. Click to show alignments

**Sequences producing significant alignments:**

	Score (bits)	E Value	
gi 9755050 gb AF269150.1 AF269150 Homo sapiens transmembran...	43	0.008	
gi 9755048 gb AF269149.1 AF269149 Gallus gallus transmembra...	43	0.008	
gi 30026031 ref NM_178146.1 Mus musculus RIKEN cDNA 181007...	43	0.008	
gi 26344651 db AK075807.1 Mus musculus 10 day old male pa...	43	0.008	
gi 22760523 db AK074824.1 Homo sapiens cDNA FLJ90343 fis...	43	0.008	
gi 6650721 gb AF116347.1 AF116347 Homo sapiens SM-11044 bin...	43	0.008	
gi 17543267 ref NM_067729.1 Caenorhabditis elegans transme...	43	0.008	
gi 14042725 db AK027788.1 Homo sapiens cDNA FLJ14882 fis...	43	0.008	
gi 19111161 ref NM_133352.1 Mus musculus RIKEN cDNA 181007...	43	0.008	
gi 13435914 gb BC004799.1 Mus musculus RIKEN cDNA 1810073M...	43	0.008	
gi 28278504 gb BC046021.1 Danio rerio, Similar to expresse...	43	0.008	
gi 9755052 gb AF269151.1 AF269151 Mus musculus transmembran...	43	0.008	
gi 7021041 db AK000756.1 Homo sapiens cDNA FLJ20749 fis...	43	0.008	

gi 18088072 gb BC020959.1 BC020959	Homo sapiens, clone MGC:...	43	0.008	
gi 24658498 ref NM_139722.2 	Drosophila melanogaster CG1059...	42	0.017	
gi 17945956 gb AY071401.1 	Drosophila melanogaster RE48767 ...	42	0.017	
gi 30681999 ref NM_100970.2 	Arabidopsis thaliana endomembr...	35	2.7	
gi 17933309 gb AF446365.1 AF446365	Arabidopsis thaliana At1...	35	2.7	
gi 20148414 gb AY081536.1 	Arabidopsis thaliana endomembran...	35	2.7	
gi 15810406 gb AY056242.1 	Arabidopsis thaliana putative en...	35	2.7	
gi 30793946 gb BT008600.1 	Arabidopsis thaliana clone U1129...	35	2.7	
gi 15451171 gb AY054666.1 	Arabidopsis thaliana endomembran...	35	2.7	
gi 17380901 gb AY063907.1 	Arabidopsis thaliana putative en...	35	2.7	

Alignments

Get selected sequences

Select all

Deselect all

☐ [gi|9755050|gb|AF269150.1|AF269150](#) Homo sapiens transmembrane protein TM9SF3 (TM9SF3) mRNA, complete cds
Length = 3592

Score = 43.1 bits (100), Expect = 0.008
Identities = 17/17 (100%), Positives = 17/17 (100%)
Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
DPSFFQHRHHWFSIFNS
Sbjct: 854 DPSFFQHRHHWFSIFNS 904

☐ [gi|9755048|gb|AF269149.1|AF269149](#) Gallus gallus transmembrane protein TM9SF3 (TM9SF3) mRNA, partial cds
Length = 234

Score = 43.1 bits (100), Expect = 0.008
Identities = 17/17 (100%), Positives = 17/17 (100%)
Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
DPSFFQHRHHWFSIFNS
Sbjct: 112 DPSFFQHRHHWFSIFNS 162

☐ [gi|30026031|ref|NM_178146.1|](#) Mus musculus RIKEN cDNA 1810073M23 gene (1810073M23Rik), mRNA
Length = 1155

Score = 43.1 bits (100), Expect = 0.008
Identities = 17/17 (100%), Positives = 17/17 (100%)
Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
DPSFFQHRHHWFSIFNS
Sbjct: 631 DPSFFQHRHHWFSIFNS 681

☐ [gi|26344651|dbj|AK075807.1|](#) Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810073M23 product:unknown EST, full insert sequence
Length = 2479



Score = 43.1 bits (100), Expect = 0.008
Identities = 17/17 (100%), Positives = 17/17 (100%)
Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
DPSFFQHRHHWFSIFNS
Sbjct: 749 DPSFFQHRHHWFSIFNS 799

☐ [gi|22760523|dbj|AK074824.1|](#) Homo sapiens cDNA FLJ90343 fis, clone NT2RP2002824, weakly similar to ENDOSOMAL P24A PROTEIN PRECURSOR
Length = 2864

Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 145 DPSFFQHRHHWFSIFNS 195

 [gi|6650721|gb|AF116347.1|AF116347](#)  Homo sapiens SM-11044 binding protein mRNA, partial cds
 Length = 1804



Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 604 DPSFFQHRHHWFSIFNS 654

 [gi|17543267|ref|NM_067729.1|](#)  Caenorhabditis elegans transmembrane protein TM9SF3 (66.6 kD), mRNA
 Length = 1743

Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 610 DPSFFQHRHHWFSIFNS 660

 [gi|14042725|dbj|AK027788.1|](#)  Homo sapiens cDNA FLJ14882 fis, clone PLACE1003537, weakly similar to ENDOSOMAL P24A PROTEIN PRECURSOR
 Length = 2459



Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +3

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 510 DPSFFQHRHHWFSIFNS 560

 [gi|19111161|ref|NM_133352.1|](#)  Mus musculus RIKEN cDNA 1810073M23 gene (1810073M23Rik), mRNA
 Length = 3143


Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 713 DPSFFQHRHHWFSIFNS 763

 [gi|13435914|gb|BC004799.1|](#)  Mus musculus RIKEN cDNA 1810073M23 gene, mRNA (cDNA clone MGC:8136 IMAGE:3589474), complete cds
 Length = 2848



Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 410 DPSFFQHRHHWFSIFNS 460

 [gi|28278504|gb|BC046021.1|](#) Danio rerio, Similar to expressed sequence AW146116, clone MGC:56246 IMAGE:5601580, mRNA, complete cds
 Length = 2082



Score = 43.1 bits (100), Expect = 0.
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 725 DPSFFQHRHHWFSIFNS 775

 >[gi|9755052|gb|AF269151.1|AF269151](#)  Mus musculus transmembrane protein TM9SF3 (Tm9sf3) mRNA, complete cds
 Length = 3143



Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 713 DPSFFQHRHHWFSIFNS 763

 >[gi|7021041|dbj|AK000756.1](#)  Homo sapiens cDNA FLJ20749 fis, clone HEP05301
 Length = 2973



Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 257 DPSFFQHRHHWFSIFNS 307

 >[gi|18088072|gb|BC020959.1|BC020959](#)  Homo sapiens, clone MGC:8842 IMAGE:3850015, mRNA, complete cds
 Length = 2870



Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 434 DPSFFQHRHHWFSIFNS 484

 >[gi|24658498|ref|NM_139722.2](#)  Drosophila melanogaster CG10590-PA [Drosophila melanogaster]
 (CG10590) mRNA, complete cds
 Length = 2663


Score = 42.0 bits (97), Expect = 0.017
 Identities = 16/17 (94%), Positives = 17/17 (100%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
 DP+FFQHRHHWFSIFNS
 Sbjct: 823 DPNFFQHRHHWFSIFNS 873

 >[gi|17945956|gb|AY071401.1](#)  Drosophila melanogaster RE48767 full length cDNA
 Length = 2662

Score = 42.0 bits (97), Expect = 0.017
 Identities = 16/17 (94%), Positives = 17/17 (100%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
 DP+FFQHRHHWFSIFNS
 Sbjct: 823 DPNFFQHRHHWFSIFNS 873

 >[gi|30681999|ref|NM_100970.2](#) Arabidopsis thaliana endomembrane protein 70, putative (Atlg10950)
 mRNA, complete cds
 Length = 2238

Score = 34.7 bits (78), Expect = 2.7

Identities = 13/17 (76%), Positives = 17 (88%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 D FF+H+HHWFSIFNS
 Sbjct: 740 DYPFFEHHQHHWFSIFNS 790

>gi|17933309|gb|AF446365.1|AF446365 Arabidopsis thaliana Atlg10950/T19D16_13 mRNA, complete cds
 Length = 2094

Score = 34.7 bits (78), Expect = 2.7
 Identities = 13/17 (76%), Positives = 15/17 (88%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 D FF+H+HHWFSIFNS
 Sbjct: 740 DYPFFEHHQHHWFSIFNS 790

>gi|20148414|gb|AY081536.1| Arabidopsis thaliana endomembrane protein EMP70 precursor isolog
 (Atlg10950) mRNA, complete cds
 Length = 1888

Score = 34.7 bits (78), Expect = 2.7
 Identities = 13/17 (76%), Positives = 15/17 (88%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
 D FF+H+HHWFSIFNS
 Sbjct: 634 DYPFFEHHQHHWFSIFNS 684

>gi|15810406|gb|AY056242.1| Arabidopsis thaliana putative endomembrane protein EMP70 precursor
 isolog (Atlg10950) mRNA, partial cds
 Length = 1650

Score = 34.7 bits (78), Expect = 2.7
 Identities = 13/17 (76%), Positives = 15/17 (88%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 D FF+H+HHWFSIFNS
 Sbjct: 251 DYPFFEHHQHHWFSIFNS 301

>gi|30793946|gb|BT008600.1| Arabidopsis thaliana clone U11293 putative endomembrane protein 70
 (Atlg10950) mRNA, complete cds
 Length = 1966

Score = 34.7 bits (78), Expect = 2.7
 Identities = 13/17 (76%), Positives = 15/17 (88%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
 D FF+H+HHWFSIFNS
 Sbjct: 634 DYPFFEHHQHHWFSIFNS 684

>gi|15451171|gb|AY054666.1| Arabidopsis thaliana endomembrane protein EMP70 precursor isolog
 (Atlg10950; T19D16.13) mRNA, complete cds
 Length = 2062

Score = 34.7 bits (78), Expect = 2.7
 Identities = 13/17 (76%), Positives = 15/17 (88%)
 Frame = +3

Query: 1 DPSFFQHRHHWFSIFNS 17
 D FF+H+HHWFSIFNS
 Sbjct: 693 DYPFFEHHQHHWFSIFNS 743

>gi|17380901|gb|AY063907.1| Arabidopsis thaliana putative endomembrane protein EMP70 precursor
 isolog (Atlg10950) mRNA, complete cds
 Length = 2113

Score = 34.7 bits (78), Expect = 2.7
 Identities = 13/17 (76%), Positives = 15/17 (88%)
 Frame = +3

Query: 1 DPSFFQHRHWFHIFNS 17
 D FF+H+HWFHIFNS
 Sbjct: 717 DYPFFEHQHWFHIFNS 767

Get selected sequences

Select all

Deselect all

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,
 or phase 0, 1 or 2 HTGS sequences)

Posted date: May 30, 2003 12:03 AM

Number of letters in database: 276,428,487

Number of sequences in database: 1,772,460

Lambda	K	H
0.337	0.144	0.553

Gapped Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 258,839,836

Number of Sequences: 1772460

Number of extensions: 955261

Number of successful extensions: 13875

Number of sequences better than 10.0: 23

Number of HSP's better than 10.0 without gapping: 13550

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 13873

length of query: 17

length of database: 2,771,168,700

effective HSP length: 0

effective length of query: 24

effective length of database: 2,771,168,700

effective search space: 66508048800

effective search space used: 66508048800

frameshift window, decay const: 50, 0.1

T: 13

A: 40

X1: 15 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 39 (21.7 bits)

S2: 73 (32.7 bits)



NCBI Nucleotide

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Books

Search for

Limits

Preview/Index

History

Clipboard

Details

Display Show: ☐ 1: AF269150. Homo sapiens tran...[gi:9755050]

Links

LOCUS AF269150 3592 bp mRNA linear PRI 09-AUG-2000
DEFINITION Homo sapiens transmembrane protein TM9SF3 (TM9SF3) mRNA, complete cds.
ACCESSION AF269150
VERSION AF269150.1 GI:9755050
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3592)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Evolution of the TM9 Super Family of Membrane Spanning Proteins
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3592)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2000) Kresge Hearing Research Institute, University of Michigan, 9301E MSRB III, 1150 West Medical Center Drive, Ann Arbor, MI 48109-0648, USA

FEATURES
source Location/Qualifiers
1..3592
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="10"
/map="10q23-q24"
gene 1..3592
/gene="TM9SF3"
CDS 218..1987
/gene="TM9SF3"
/note="transmembrane protein 9 superfamily member 3"
/codon_start=1
/product="transmembrane protein TM9SF3"
/protein_id="AAF98159.1"
/db_xref="GI:9755051"
/translation="MRPLPGALGVAAAAALWLLLLLPRTRADEHEHTYQDKEEVVLW
MNTVGPYHNRQETKYFSLPFCVGSKKSI SHYHETLGEALQGVLEFSGLDI KFKDDV
MPATYCE IDLDKEKRDFAVYAIKNHYWYQMI IDDLPIWGI VGEADENGEDYYLWTKK
LEIGFNGNRIVDVNLTSEGVKLVNPTKI QISYSVKWKKSDVKFEDRFKYLDPSFFQ
HRIHWFSIFNSFMMVIFLVGLVSMILMRTLKDYARYSKEEEMDDMDRLDGEYGWKO
VHGDVFRPSSHPLIFSSLIGSGCQIFAVSLI VIVAMIEDLYTERGSM LSTAI FVYAA
TSPVNGYFGGSLYAROGGRRWIKQMF IGAFI PAMVCGTAFF INFIAIYYHASRAIPF
GTMVAVCCICFFVILPLNLVGTILGRNLSGQPNPCRVNAVPRPIPEKKWFMEPAVIV
CLGGILPFGSIFIEYMFIFTSFWAYKIYYVYGFMMVLVLVILCIVTVCVTIVCTYFLN
AEDYRQWTSFLSAASTAIYVYMYSFYFFYFKTKMYGLFQTSFYFGYMAVFSTALGIM
CGAIGYMGTSFAVRKIYTNVKID"

BASE COUNT 1026 a 604 c 815 g 1147 t
ORIGIN

```
1 gaggaagagg ctgaggagcg gceggggggc ggggaggctc aggaagcgcc ggtgacggcg
61 acggcgggcg cagaggagcg agcgcgctgg cggggccccc tgcgtctgtc cgcggcccggt
121 ggatgcgaat cggcgcgccg ggaggcgccg gcggcgagg agggcgccgc gggaggagga
181 gtcggtgagc cggctcggcg cgggagggcg gcggaggatg aggcggctgc ctggcgctct
241 tggcggtggc gcggcgcccg cgtgtggct gctgctgctg ctgctgccc ggacccggcg
301 ggacgagcac gaacacacgt atcaagataa agaggaaagt gtcttatgga tgaatactgt
361 tgggcccac cataatcgct aagaacata taagtacttt tcacttccat tctgtgtggg
421 gtcaaaaaaa agtatcagtc attaccatga aactctggga gaagcacttc aaggggttga
481 attggaattt agtggctcgg atattaaatt taaagatgat gtgatgccag ccacttactg
541 tgaattgat ttagataaag aaaagagaga tgcatttgta tatgccataa aaatcatta
601 ctggtaccag atgtacatag atgatttacc aatatggggt attgttggtg aggotgatga
661 aaatggagaa gattactatc ttggaccta taaaaaactt gaaataggtt ttaatggaaa
721 tcgaattgtt gatgttaatc taactagtga aggaaggtg aaactgggtc caaatactaa
781 aatccagatt tcatattcag taaaatggaa aaagtcagat gtgaaatttg aagatcgatt
841 tgacaaatat cttgatccgt ccttttttca acatcggatt cattggtttt caattttcaa
901 ctcttctcat atggtgatct tottggtggg cttagtttca atgattttaa tgagaacatt
961 aagaaaagat tatgctcggt acagtaaaga ggaagaaatg gatgatattg atagagacct
1021 aggagatgaa tatggatgga aacagggtgca tggagatgta tttagaccat caagtcaccc
1081 actgatattt tctctctgta ttggttctgg atgacagata ttgctgtgt ctctcatcgt
1141 tattattgtt gcaatgatag aagatttata tactgagagg ggaatcaatgc tcagtacagc
1201 catatttgct tatgctgcta cgtctccagt gaatggttat ttggaggaga gtctgtatgc
1261 tagacaagga ggaaggagat ggataaagca gatgtttatt ggggcattcc ttatccagag
```

1321 tatggtgtgt ggcactgcct tottca tttcatagcc atttattacc atgcttcaag
1381 agccattcct tttggaacaa tgggtggcgt ttgttgcatc tgtttttttg ttattcttcc
1441 totaaatott gttggtacaa tacttgccg aaatctgtca ggtcagccca actttccttg
1501 tegtgtcaat gctgtgcctc gtctataacc ggagaaaaaa tggttcatgg agcotgagg
1561 tattgtttgc ctgggtggaa ttttaccttt tggttcaatc ttatttgaat tgtatttcat
1621 cttcacgtct tctggggcat ataagatcta ttatgtctat ggcttcatga tgcgtgtgct
1681 ggttatcctg tgcattgtga ctgtctgtgt gactattgtg tgcacatatt ttctactaaa
1741 tgcagaagat tacgggtggc aatggacaag tttctctctc gctgcatcaa ctgcaatcta
1801 tgtttacatg tattcctttt actactattt tttcaaaaca aagatgtatg gcttatttca
1861 aacatcattt tactttggat atatggcggg atttagcaca gccttgggga taatgtgtgg
1921 agcgattggg tacatgggaa caagtgcctt tgtccgaaaa atctatacta atgtgaaaaa
1981 tgactagaga cccaagaaaa cctggaactt tggatcaatt tctttttcat aggggtggaa
2041 cttgcacagc aaaaacaac aaacgcaaga agagatttgg gctttaacac actgggtact
2101 ttgtgggtct ccttttctgc ggtggcttaa agtaacatct atttccattg atcctagggt
2161 cttcctgact gctttctcca actgttcaca gcaaatgctt ggattttatg cagtaggcac
2221 tactacagta catgggtaat cttcccaaaa actagctcat taaagatgaa atagaccagc
2281 tctcttcagt gaaggaggaca aatagtttat ttaaagcatt tgttccaata aaataaatag
2341 agggaaaactt ggatgctaaa attacatgaa taggaatctt cctggcactt agtgtttcta
2401 tgttattgaa aaatgatgtt ccagaaagat tacttttttc cttctatttt tactgccatt
2461 gtgcacctat tgtgggacat ttttatatat tgaatctggg tttctttttg actttttttt
2521 ttcccaatcc aacagcatcc ttttttttaa aagagagaat tagaaaaat taaatcctgc
2581 atgtaataata tctgtctgca tottagttgg accaacttcc catttatita tcttaaaact
2641 atacagttac atcttaattc catccaaaaga agatacagtt tgaagacaga agtgactctt
2701 ctacaatgca atttactgta cagttagaaa gcaaatgttt aaatggagaa gatacttgtt
2761 tttattaaac attttgagat ttagataaac tacattttta ctgaatgtct aaagtgatta
2821 tcttttttcc ccccaagtta gtcttaaatc ttttgggttt gaatgaaggt tttacataag
2881 aaattattaa aaacaagggg ggtgggtaat aaatgtatat aacattaaat aatgtaacgt
2941 aggtgtagat tcccaaatgc atttggatgt acagatcgac tacagagtac tttttctta
3001 tgatgatgtg ttagaaaatg tgtgatttgg gtgggctttt acatcttgcc taccattgca
3061 tgaacacattg ggttttcttc aaaatgtgtg tgtcataact cttttgggag ggggggtgtt
3121 ttctttctgtt tattttctga gactcctaca ggagccaaat ttgtaattta gagacactta
3181 attttgttaa tctgtcttgg gacacttaag taacatctaa agcattattg ctttagaatg
3241 ttcaaaaaaa atttctgtac caaattgttt tgtggaaata gatgtgttg caatttgaag
3301 atatctttct gtccagaagg caaaattacc gaatgccatt tttaaaagta tgcataaac
3361 tatgtctact tcatacaggg gaccogtatt ttaaaatctc cagacttgct tacatctaga
3421 ttatccagca caatcataaa gtgaatgaca aacoccttga atgaaattgt ggcacaaaat
3481 ctgttcagggt tgggtgaccg tgaagtgg ggatgggta aaagtgtta acgtactgtt
3541 ggatcaacaa ataaaggtta cagttttgta agagaaaaaa aaaaaaaaaa aa

//

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

May 20 2003 11:20:17



Nucleotide

PubMed

ನಿರ್ದೇಶಕರು

Protein

Genetics

Structure

PRAC

13x of 3m.y

Q34M

Rocks

Search for

Limits

[Preview/Index](#)

History

Clipboard

Details

Display Show: Send to Get Subsequence

☐ 1: AF269149. Gallus gallus tra...[gi:9755048]

Links

LOCUS	AF269149	234 bp	mRNA	linear	VRT 09-AUG-2000
DEFINITION	Gallus gallus transmembrane protein TM9SF3 (TM9SF3) mRNA, partial cds.				

ACCESSION AF269149
VERSION AF269149.1 GI:9755048

KEYWORDS .
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Archosauria: Aves: Neognathae: Galliformes: Phasianidae:
Phasianinae: Gallus.

REFERENCE 1 (bases 1 to 234)
AUTHORS Gong, T. W., Hegeman, A. D., Shin, J. J., Adler, H. J., Raphael, Y. and Lomax, M. I.

TITLE Identification of genes expressed after noise exposure in the chick
basilar papilla

JOURNAL Hear. Res. 96 (1-2), 20-32 (1996)

MEDLINE 96414275

PUBMED 8817303

REFERENCE 2 (bases 1 to 234)

AUTHORS Warner, S. J. and Lomax, M. I.

TITLE Evolution of the TM9 Super Family of Membrane Spanning Proteins

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 234)

AUTHORS Warner, S. J. and Lomax, M. I.

TITLE Direct Submission

JOURNAL · Submitted (10-MAY-2000) Kresge Hearing Research Institute,
University of Michigan, 9301E MSRB III, 1150 West Medical Center
Drive, Ann Arbor, MI 48109-0648, USA

```

FEATURES             Location/Qualifiers
     source           1..234
                        /organism="Gallus gallus"
                        /mol_type="mRNA"
                        /db_xref="taxon:9031"
                        /tissue_type="basilar papilla"

```

gene <1..>234

/gene="T

CDS <1..>234

```

/ gene="TM9SF3"
/ note="transmembrane protein 9 superfamily member 3"
/ codon_start=1
/ product="transmembrane protein TM9SF3"
/ protein_id="AAF98158.1"
/ db_xref="GI:9755049"
/ translation="ASEGKVKLVPTNTKIQMSYMKWKKSVDKVFEDRFDKYLDPSFFQH
RIHWFSIFNSFMNVIFLVLGVSLMLRTRLRKKK"

```

BASE COUNT	80 a	38 c	46 g	70 t
ORIGIN				

```

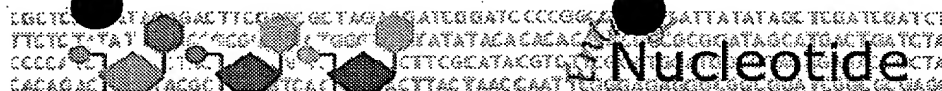
1 gccagcgaag gaaaggtgaa actgttaca aatacaaaaa tccagatgto atattctatg
61 aagtggaaga agtcagatgt gaaatttgaa gaccgatttg acaagtaacct tgaccatctt
121 ttctttcaga acagaattca ctggttttca attttcaatt ctttcgatgt ggtgatcttt
181 ctggtttggc tagtgcctat gtattaatg agaactttgc gaaaaaaaaa aaaa

```

//

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

May 20 2003 11:20:12



Search for

Display Show:

☐ 1: NM_178146. Mus musculus RIKE...[gi:30026031]

LOCUS 1810073M23Rik 1155 bp mRNA linear ROD 18-MAY-2003
DEFINITION Mus musculus RIKEN cDNA 1810073M23 gene (1810073M23Rik). mRNA.
ACCESSION NM_178146
VERSION NM_178146.1 GI:30026031
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1155)
AUTHORS Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,

Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,
Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,
McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,
Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,
Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,
Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M.,
Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E.,
Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.

TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 1155)

AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusica, V.,
Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawaji, H., Kawasaki, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

REFERENCE 3

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from AK075807.1.

FEATURES
source
1..1155
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="19"
gene
1..1155
/gene="1810073M23Rik"
/note="synonyms: SMBP, Tm9sf3, 2810031D16Rik"
/db_xref="LocusID:107358"
/db_xref="MGI:1914262"
CDS
1..1155
/gene="1810073M23Rik"
/note="putativeunknown EST (GB|BGO73434, evidence: BLASTN,
99%, match=803): SM-11044 binding protein"
/codon_start=1
/product="transmembrane protein 9 superfamily member 3"
/protein_id="NP_835359.1"
/db_xref="GI:30026032"
/db_xref="LocusID:107358"
/db_xref="MGI:1914262"
/translation="MRPLPGAPGVAAAAALLLLPRARSDEHEHTYQDKEEVVLWMN
TVGPYHNROQETKYFSLPFCVSGSKKSIHYHETLGEALQGVLEFSGLDIKFKDDVMP
GTyceIDLDEKRDFAFYAIKNHYWYQMYIDDLPIWGIVGEADENGEDYLLWYKKLE
IGFNGNRIVDNLTSSEKVKLVPTNKIQMSYSVKWKKSDVKFEDRFDKYLDPSFFQHR
IHWFSIFNSFMVMVIFLVGLVSMILMRTLKDYARYSKEEEMDDMDRLGDEYGWKQVH
GDVFRPSSHPLIFSSLIGSGCQIFAVSLIVIVAMIEDLYTERGSMLSLIFVYAATS
PVNGYFGGSLYARQGGRRWIKDVYRGIPYPSYGVWHCILHQLYSHLLPCL"
misc_feature
160..1071
/gene="1810073M23Rik"
/note="ENP70: Region: Endomembrane protein 70"
/db_xref="CDD:pfam02990"

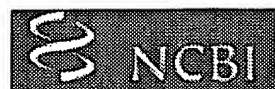
BASE COUNT 340 a 199 c 278 g 338 t
ORIGIN

```
1 atgaggcgcg tgcggcgcg tctggcggtg gcgggcgccg cgcggttgtt gttgctgctg
61 ctgccccggg ctgcgtctga cgagcacgaa cacacgtatc aagataaaga agaagttgtt
121 ttatggatga atactgttgg gccctaccac aatcgccaag aaacataaa atacttttca
181 cttcattctt gtgtgggggc aaaaaaaagt atcagtcatt accatgaaac tttgggagaa
241 gcacttcaag gaggttgaat agaatttagt gccctggaca ttaaatttaa agatgatgtg
301 atgccaggca ctactgtga aattgactta gataaagaga agagagatgc gtttgtgtat
361 gctatcaaga atcactattg gtatcagatg tacatagatg acttaccat atgggggtatt
421 gttggtgaag cagatgaaaa tggggaagat tactatcttt ggacctacaa aaaacttgaa
481 ataggcttta atggaaatcg aattgttgat gttaatctaa ctagtgaagg aaaggtaaa
541 ctggttccaa atactaaaat acagatgtca tattcggtaa aatggaaaaa atcggatgta
601 aaatttgaag atcgatttga taaatatctt gatccatcct tttttcagca taggattcac
661 tggttttcaa tttttaattc cttcatgatg gtgatcttct tagtgggatt agtttcaatg
721 attttaatga gaactttaag gaaagattat gcccgataga gtaaagaaga agaatggat
781 gacatggaca gagacctagg agacgagtat ggctggaagc aggtgcatgg agatgtgttc
841 agaccgtcaa gtcacctctt gatcttctcc tccctcattg gctctggatg tcagatattt
901 gctgtgtctc tcattgttat tattgttgcc atgatatagg acttatatac agagaggggg
961 tcaatgctca gcacagccat atttgtctat gctgctacat cgccagtga cgggtacttt
1021 ggaggaagtc tgtatgctag acaaggagga aggagatgga taaaggatgt ttatcggggc
1081 attccttacc ccagctatgg tgtgtggcac tgcattcttc atcaacttta tagccattta
1141 ttaccatgcc tctag
```

//

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

May 20 2003 11:20:17



NCBI Nucleotide

Search for

Display Limits Show:

History Clipboard Details

☐ 1: AF116347. Homo sapiens SM-1...[gi:6650721]

LOCUS AF116347 1804 bp mRNA linear PRI 16-OCT-2001
DEFINITION Homo sapiens SM-11044 binding protein mRNA, partial cds.

ACCESSION AF116347

VERSION AF116347.1 GI:6650721

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1804)

AUTHORS Sugawara, T., Lenzen, G., Simon, S., Hidaka, J., Cahen, A.,
Guillaume, J.L., Camoin, L., Strosberg, A.D. and Nahmias, C.

TITLE The iodocyanopindolol and SM-11044 binding protein belongs to the
TM9SF multispansing membrane protein superfamily

JOURNAL Gene 273 (2), 227-237 (2001)

MEDLINE 21479397

PUBMED 11595169

REFERENCE 2 (bases 1 to 1804)

AUTHORS Sugawara, T., Lenzen, G., Simon, S., Hidaka, J., Cahen, A.,
Guillaume, J.L., Camoin, L., Nahmias, C. and Strosberg, A.D.

TITLE Direct Submission

JOURNAL Submitted (23-DEC-1998) Vetigen, 21 rue Sebastien Mercier, Paris
75015, France

FEATURES

source

Location/Qualifiers

1..1804

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="skeletal muscle"

CDS

<1..1737

/note="contains nine potential membrane spanning domains:
similar to yeast EMP70 protein precursor encoded by
GenBank Accession Numbers X67316 and S25110"

/codon_start=1

/product="SM-11044 binding protein"

/protein_id="AAF21983.1"

/db_xref="GI:6650722"

/translation="AAAALWLLLLLPRTRADEHEHTYODKEEVVLMNVTGVPYHNRO
ETKYFSLPFCVGSKKISHYHETLGEALQVELEFSGLDIKFKDDVMPATYCEIDLD
KEKRDFAFYVAIKNHYYQMYIDDLPIWGIWGEADENGEDYLLWYKKLEIGFNGNRIV
DVNLTSEGVKLVLPNTKIQMSYSVKWKKSDVKFEDRFDKYLDPSFFQHRHWFISFNS
FMVMVIFLVGLVSMILMRTLKDYARYSKEEEMDDMDRLGDEYGWKQVHGDVFRPSSH
PLIFSSLIGSGCQIFAVSLIVIVAMIEDLYTERGSMLSLTAIFYAATSPVNGYFGGS
LYARQGGRRWIKQMFIGAFLIPAMVCGTAFFINFIAIYYHASRAIPFGTMVAVCCICF
FVILPLNLVGTILGRNLSGPNFPCRVNAVPRPIPEKKWFMEPAVIVCLGGILPFGSI
FIEMFYIFTSFWAYKIYYVYGFMMMLVLVILCIVTVCVTIVGTYFLLNAEDYRWQWTSF
LSAASTAIYVYMYSFYFFYFKTKMYGLFQTSFYFGYMAVFSTALGIMCGAIGYMGTS
FVRKIYTNVKID"

BASE COUNT 509 a 301 c 403 g 591 t
ORIGIN

```
1  gcggccgcgc  cgtgtggt  gctgtgtg  ctgctgccc  ggaccgggc  ggaagagcac
61  gaacacacgt  atcaagataa  agaggaagt  gtcttatga  tgaatactgt  tgggccctac
121  cataatcgct  aagaaacata  taagtacttt  tcacttccat  tctgtgtggg  gtcaaaaaaa
181  agtatcagtc  attaccatga  aactctggga  gaagcacttc  aagggttga  attggaattt
241  agtggctctg  atattaaatt  taaagatgat  gtgatgccag  ccacttactg  tgaattgat
301  ttagataaag  aaaagagaga  tgcatttgta  tatgccataa  aaatcattta  ctgtaccag
361  atgtacatag  atgatttacc  aatatggagt  attgttggtg  aggtgatga  aaatggagaa
421  gattactatc  ttggacccta  taaaaaactt  gaaataggtt  ttaattgaaa  tgaattgtt
481  gatgttaatc  taactagtga  aggaaggtg  aaactggttc  caaatactaa  aatccagatg
541  tcatattcag  taaaatggaa  aaagtcagat  gtgaaattg  aagatcgatt  tgacaaatat
601  cttgatcgct  ccttttttca  acatcggatt  cattgtttt  caattttcaa  ctccttcag
661  atggtgatct  tctgtgtggg  cttagtttca  atgattttaa  tgagaacatt  aagaaaagat
721  tatgctcggt  acagttaaga  ggaagaaatg  gatgatattg  atagagacct  aggagatgaa
781  tatgatgga  aacaggtgca  tggagatgta  tttagaccat  caagtcacc  actgatattt
841  tctctctgta  ttggtctgga  atgtcagata  tttgtgtgt  ctctcatcgt  tattattgtt
901  gcaatgatag  aagatttata  tactgagagg  ggatcaatgc  tcagtacagc  catatttgc
961  tatgtctgta  cgtctccagt  gaatggttat  tttggaggaa  gtctgtatgc  tagacaagga
1021  ggaaggagat  ggataagca  gatgtttatt  gggcattcc  ttatccagc  tatggtgtg
1081  ggcactgcct  tcttcatcaa  ttcatagcc  atttattacc  atgcttcaag  agccattcct
1141  ttggaacaa  tgggtgccgt  ttgttcac  tgttttttg  ttattcttc  tctaattctt
1201  gttgtacaa  tacttgccg  aaatctgtca  gtcagccca  acttctctg  tctgtcaat
```

```
1261 gctgtgctc gtcctatacc ggag      a tggttcatgg agoctgcggt tattgtttgc
1321 ctgggtggaa ttttacottt tggttcaatc ttattgaaa tgtatttcat cttcacgtct
1381 ttctgggcat ataagatcta ttatgtctat ggcttcatga tgcgtgtgct ggttatcctg
1441 tgcattgtga ctgtctgtgt gactattgtg tgcacatatt ttctactaaa tgcagaagat
1501 taccggtggc aatggacaag tttctctct gctgcatcaa ctgcaatcta tgtttacatg
1561 tattcctttt actactattt ttcaaaaaca aagatgtatg gcttatttca aacatcattt
1621 tactttggat atatggcggt atttagcaca gccttgggga taatgtgtgg agcgattggt
1681 tacatgggaa caagtgcctt tgtccgaaaa atctatacta atgtgaaaat tgactagaga
1741 cccaagaaaa cctggaactt tggatcaatt tctttttcat aggggtggaa cttgcacagc
1801 aaaa
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

May 20 2003 11:20:12



NCBI Nucleotide

Search for

Display Limits Show: Preview/Index History Details

1: NM_067729. Caenorhabditis el...[gi:17543267]

LOCUS 4C515 1743 bp mRNA linear INV 22-NOV-2002

DEFINITION Caenorhabditis elegans transmembrane protein TM9SF3 (66.6 kD), mRNA.

ACCESSION NM_067729

VERSION NM_067729.1 GI:17543267

KEYWORDS

SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

COMMENT VALIDATED REFSEQ: This record has undergone preliminary review of the sequence, but has not yet been subject to final NCBI review. The reference sequence was derived from WormBase CDS:Y41D4A.4. Fully supported by cDNA from the Worm Transcriptome Project. COMPLETENESS: full length.

FEATURES

source

Location/Qualifiers

1..1743

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/db_xref="taxon:6239"

/chromosome="IV"

/map="IV:-15.38 cM (interpolated genetic position)"

/map="IV: covering 5823 bp. from base 1745879 to 1751703 on genome release WS85"

/clone="Primers to amplify the CDS (Stop included):

ATGCGGGTACTGATAAGCC (T=57.6).

TTAATCGATTTTCACAGTCTGATAGATT (T=56.4)"

/clone_lib="[Predicted cellular localisation] PSORT II analysis. (K. Nakai) trained on yeast data predicts that the subcellular location of this protein is most likely in the endoplasmic reticulum (66%) or in the plasma membrane (33%)."

gene

1..1743

/gene="4C515"

/locus_tag="4C515"

/note="synonyms: Y41D4A.4, CELK01378"

CDS

1..1743

/gene="4C515"

/locus_tag="4C515"

/function="Transporter GO:0005215 [Pfam/Interpro/GO]"

/function="Transport GO:0006810 [Pfam/Interpro/GO]"

/function="Integral membrane protein GO:0016021

[Pfam/Interpro/GO]"

/note="|| [Common ancestor, from TaxBlast with threshold

10-3] Eukaryota || [Closest homologs] Dictyostelium

discoideum: emb|CAC47950.1| (score=271); Arabidopsis

thaliana: ref|NP 563881.1| (528); Saccharomyces

cerevisiae: ref|NP 010392.1| (211); Schizosaccharomyces

pombe: ref|NP 596464.1| (177); Caenorhabditis elegans:

ref|NP 500130.1| (1028); Anopheles gambiae str PEST:

gb|EAA09712.1| (724); Drosophila melanogaster: ref|NP

647979.1| (728); Mus musculus: ref|NP 579930.1| (760);

Homo sapiens: ref|XP 050993.1| (761)"

/codon_start=1

/product="Transmembrane protein TM9SF3 (66.6 kD)"

/protein_id="NP_500130.1"

/db_xref="GI:17543268"

/db_xref="AceView/WormGenes:4C515"

/db_xref="CDD:pfam02990"

/db_xref="LocusID:176983"

/db_xref="NextDB:CELK01378"

/db_xref="WormBase:Y41D4A.4"

/translation="MRVLISLLFTSLLEADEHDHLYEVD EEVVLMNTVGPYSNRQ
ETTYFSLPFCCKGEKKEIGHYHETMGESLLGVELEFSGLDIKFRNTTKTKTVVCKKLT
ETDYKTLLEYAIQNSYYYQMYLDDMPIWGMVGEIDNTVNPPAYKLYTHKRDLIGYNDKQ
VVDVNLITDGRVDIRPGAELFTYEVQWSKSEVDFTKRFDKYLDPSFFQHRHWFISIF
NSFMNVVFLVGLVWMILVRTLKDYARYQKEDSLDLDADLGDEYGWKQVHGDVFRPP
SMPLLFSSCIGAGYHFTVAVITLAI VGEFYTERGSLLSAAIFVYAACPVPNGYAG
GSMYARFGGRHWIKQMLLGAFLLPSMVCVGAFLINFIAYYASRAIPFTIMLAVSAI
CLFVILPLTLVGTIVGRNMAGSADYPCRVNAVPRIPDKKWFVQVPLITLAGGVLPFG
SIFIMFYIFTFWAYKIYVYVGFMLLVTIILSIVTVCVTVCSYFLLNAEDYRWRWT

SFACGASTAFYVYMY...FFKTKMYGLFQTVFYFGYMGIFAAALGLMTGTIGYVGT
AKFVRKIYQTVKID~

misc feature 1..51
/gene="4C515"
/locus_tag="4C515"
/note="Region: [PSORT] N terminal signal domain"

misc feature 133..1614
/gene="4C515"
/locus_tag="4C515"
/note="Region: [Pfam/InterPro description] endomembrane protein 70: the transmembrane 9 superfamily protein (TM9SF) may function as a channel or small molecule transporter. Proteins in this group are endosomal integral membrane proteins. HMMER score 820.10 Eval=5.1e-244"
/db_xref="CDD:pfam02990"

misc feature 658..708
/gene="4C515"
/locus_tag="4C515"
/note="Region: [PSORT] transmembrane domain: SFMMVVFLVGLVWMILV"

misc feature 874..924
/gene="4C515"
/locus_tag="4C515"
/note="Region: [PSORT] transmembrane domain: VFTVAVITTLAIVGEF"

misc feature 937..987
/gene="4C515"
/locus_tag="4C515"
/note="Region: [PSORT] transmembrane domain: GSLLSAAIFVYACSPV"

misc feature 1054..1104
/gene="4C515"
/locus_tag="4C515"
/note="Region: [PSORT] transmembrane domain: LGAFLLPSMVGVAFLLI"

misc feature 1159..1209
/gene="4C515"
/locus_tag="4C515"
/note="Region: [PSORT] transmembrane domain: LAVSAICLFVILPLTLV"

misc feature 1312..1362
/gene="4C515"
/locus_tag="4C515"
/note="Region: [PSORT] transmembrane domain: WLITLAGGVLPFGSIFI"

misc feature 1426..1476
/gene="4C515"
/locus_tag="4C515"
/note="Region: [PSORT] transmembrane domain: LLVTIILSIVTVCVTIV"

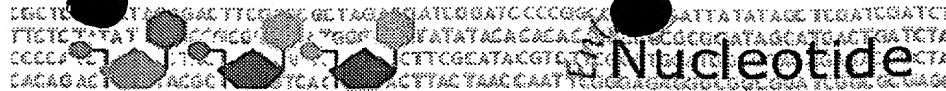
misc feature 1726..1737
/gene="4C515"
/locus_tag="4C515"
/note="Region: [PSORT] ER membrane domain: TVKI"

BASE COUNT 442 a 428 c 404 g 469 t
ORIGIN

```
1 atcggggtac tgataagcct gctactatc accctcgctc togtcgaagc cgacgaacac
61 gaccatttgt acgaggtcga cagaggaggt gtattatgga tgaacacggt gggaccctac
121 tgaatcgcc aggaaaccta cactacttc tccctgccat ttgttaaagg agagaagaag
181 gaaattggcc attatacaga aactatggga gaatcactgc tcggcgtgga gctagagttc
241 tccggattgg atataaaatt cagaacaac accaagaaaa ccgtggtttg cgagaagaag
301 ctcaccgaaa ccgactataa aacgctgctc tacgctatcc aaaacagcta ttactatcaa
361 atgtacctcg acgacatgcc gatttgggga atggttgagg aaatcgataa tactgtgaat
421 ccgccggcct acaagcttta tacgcataag aggttagata ttggctataa cgataagcag
481 gtgttcgacg tgaatttgac aacagacgga agagttgata ttgctccggc cgtgagctc
541 acgttcacct atgaggtgca atggagcaag tcggaagtgg attttaccaa gagattcgat
601 aaatatctcg atccaagctt ctccagcac agaattccact ggttctcgat ttttaacagt
661 ttcatgatgg tcgtattcct cgtcggattg gtaggatga ttctagtcgg tactctacga
721 aaagactacg ccgcatacca aaaagaggat agtctcgacg atttggacgc cgtatcggga
781 gatgagtacg gttggaacaa ggttcacgga gacgtcttcc gtccaccatc aatgocgttg
841 ctcttctcat cgtgtatttg agccggttat catgtgttca ctgtcgcggt tattacgacg
901 attttggcga ttgttgagga attttataca gaacgcggct ccctactctc cgcgcgaatc
961 ttgctctacg ccgcttgctc gccagtcaac ggaatgcggc gcggatcgat gtacgccaga
1021 ttccggagtc gtcactggat caagcaaatg ctctcggag cattccttct gccaaagtatg
1081 gtgtgtggtg tcgcattcct tatcaacttt atcgcgatct actatcacgc gtcacgcgcc
1141 attccattca caattatgct cgcgctctcg gcgatctgcc tctttgtgat ccttcgcgtg
1201 actcttgtcg gaactgtgat cggaagaagt atggctggaa gtgcagacta tccgtgtaga
1261 tgaatgcgag tcgcagagac cattcctgat aagaaatggt tcgtccaacc gtggctcatc
1321 acccttgccg gaggtgttct ccattcggga tccatcttca tcgaaatgta ctttatcttc
1381 accctattct gggcgtacaa aatctattat gtgtacggat tcatgotttt ggtcacaaata
1441 atoctgtcaa ttgtcacogt atgogtcaca attgtctgct cctacttctc actcaacgcc
1501 gaggattata gatggagatg gacgagcttc gcgtgtggag catctactgc attctatgtg
1561 tacatgtatt ccatgtatta ttcttcttc aagacaaaaa tgtacggact ttcccaaacg
1621 gtcttctact ttggatacat gggaatcttc gccgccgctc tcggactcat gaccggcacc
1681 atcggatacg tcggaaccgc caaatctgct cgcacaaatct atcagactgt gaaaatcgat
1741 taa
```

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

May 20 2003 11:20:12



Search for

Display Show:

☐ 1: BC046021. Danio rerio, Simi...[gi:28278504]

LOCUS BC046021 2082 bp mRNA linear VRT 10-FEB-2003
DEFINITION Danio rerio, Similar to expressed sequence AW146116, clone
MGC:56246 IMAGE:5601580, mRNA, complete cds.
ACCESSION BC046021
VERSION BC046021.1 GI:28278504
KEYWORDS MGC.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 2082)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Sumio Sugano
cDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 103 Row: 1 Column: 14.

FEATURES
source
1..2082
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="MGC:56246 IMAGE:5601580"
/tissue_type="Whole body, adult male"
/clone_lib="Sugano_SJD_adult_male"
/lab_host="DH10B"
/note="Vector: pME18S-FL3"
CDS
98..1858
/codon_start=1
/product="Similar to expressed sequence AW146116"
/protein_id="AAH46021.1"
/db_xref="GI:28278505"
/translation="MGLCKWTFEVVALTAVFSSFIPVRADEHEHKYTDKEEVLWMNT
VGPYHNRQETKYFSLPFCVGTKKTI SHYHETLGEALOGVELEFSGLDIKFKEEVLQT
TYCDIELDKPKRDAFYAIKNHYWYQYIDDLPIWGI VGEADENGEDYYLWTKKLEI
GHNGNRIVDVNLTSSEKVKLVNTRIPMSYSVKWKKSDVKFEDRFDKYLDPSFFQHR
HWFIFNSFMVIFLVGLVSMILMRTLKDYARYSKEEEMDDMDRDPGEYGWKQVHG
DVFRRPSSHPLIFSSLIGSGCQIFSVSLVILAMIEDLYTERGSLSTAIFVYAATSP
VNGYFGGSLYAKGGRRWIKQMFIGAFLIPAMVCGTAFFINFIAYHASRAIPFGTM
VAVCCICLFVILPLNLVGTILGRNLSGQPNFPCRVNAVPRPIPEKKWFMEPAVIVCLG
GILPFGSIFIMFYIFTSFWAYKIYVYGFMMMLVLVILCIVTVCVTIVCTYFLLLNAED
YRWQWTSFLSAASTAVYVYMSFYFFFKTKMYGLFQTSFYFGYMAVFSTALGIMGGA
VGYMGTSFAVRKIYTNVKID"

BASE COUNT 601 a 424 c 478 g 579 t
ORIGIN

```
1 aagacaacca ctgtcataga accaggaaga aggaaggtgg gatagcccc aaaagatac
61 catttcaaat cagtgcaga attttcccta gaaacccatg ggcctctgca agtggacgtt
121 tgaagtgtgt gccttgacgg ctgtttttag ttctgtcata ccagttcgag cagatgaaca
181 cgagcacaag tacacagata aagaagaggt ggttttatgg atgaatacag tgggccctta
241 tcacaaccga caggagacct ataagtactt ctccctaccg ttctgtgtgg gaacgaaaaa
301 aactattagt cattatcatg agacattagg agaggcgcta caggggttg aattggagtt
361 cagcggcttg gacatcaagt taaaagagga ggtgttcag acgacatact gtgacattga
421 actagacaaa cctaaaagag atgcatttgt ctatgccatc aagaacct actggtacca
481 aatgtacata gatgacctc coactctggg aattgttgt gaagctgatg agaattggaga
```


541 ggactattac ctttggactt acaaa ggagatcgga cataatggga acagaattgt
601 ggatgttaac ctaaccagtg agggcaaggt taagcttggt ccaaacacga gaattcccat
661 gtcatactct gtaagtgga agaaatctga tgtgaaattt gaggatagat ttgacaaata
721 cottgatcca tctttctttc aacacagaaat tcactgggtc tcaatattca actcattcat
781 gatggtgatt ttcttgggtg gccttgttgc aatgatcctg atgagaacat taaggaaaga
841 ctatgccaga tacagcaaag agggagaaat ggatgacatg gatcgtgato ctggtgatga
901 atatggctgg aagcaggttc acggggatgt gttcaggcca tccagtccac cgctgatctt
961 ctctcccttc attggctctg gctgtcaaat tttttcagtt tcccttatag tcataatttt
1021 ggccatgatt gaggacttgt atacagagag aggggtccatg ttgagtacag ccatatttgt
1081 ttatgctgcc acgtctccag tcaatggcta ctttgggtga agcctatatg caaaacaagg
1141 agggagaaga tggataaagc agatgttcat tggagccttc ctgattcctg caatgggtgtg
1201 tggtagacgg tttttcatca acttcacgc catctactac catgcctcaa gagcaatccc
1261 attcggcact atgggttgcg tgtgctgcat ctgcttattt gtaattctac ctctgaacct
1321 ggtggggacg atcctgggca gaaacctctc cggacagccc aactttcctt gtagagtcaa
1381 tgcgtgaccc agaccatcc cagaaaagaa atggtttatg gagccagcag ttatcgtgtg
1441 tttaggtggc atcctccatc tcggctcgat attcattgaa atgtacttca ttttcacatc
1501 tttctgggcc tacaagattt actatgtgta tggatttatg atgctggtgc tgggtgatct
1561 gtgcacgttt actgtctgag tcaccattgt ctgcacctac ttcttctca atgcagaaga
1621 ctacagatgg cagtggacaa gctttctctc tgcagcgta acagcagttt atgtttacat
1681 gtactccttc tactactatt tcttcaaac aaagatgtat ggcttattcc agacgtcatt
1741 ctactttggc tacatggctg tgttcagcac tgctctggga atcatgtgtg gagcgggtgg
1801 ttacatggga acaagtgcct ttgtgaggaa gatctacaca aatgtgaaaa tcgactaaaa
1861 ctctgcagag acgcagcaga agagccgaca ctctctccc atcgaaacgg gcacaaagtc
1921 tccatttatt ttgcaagatg agattgtggt atcttgtaca aaatctagtt ttccattttc
1981 tcaatgaatt aaacgttgcg gcatgatgca tacacaaggg taaaccgaga gggttaataa
2041 acaggacttt taattttaaa aaaaaaaaaa aaaaaaaaaa aa

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

May 20 2003 11:20:17



results of BLAST

TBLASTN 2.2.6 [Apr-09-2003]

Seq ID No. 6

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

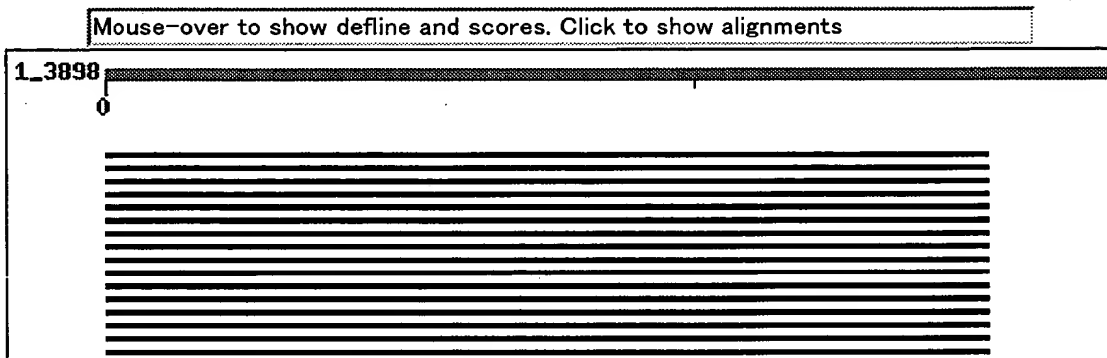
RID: 1054282789-05952-1524

Query=

(17 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
1,772,460 sequences: 8,313,506,101 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Taxonomy reportsDistribution of 16 Blast Hits on the Query Sequence

Sequences producing significant alignments:

	Score (bits)	E Value	
gi 9755048 gb AF269149.1 AF269149 Gallus gallus transmembra...	<u>35</u>	2.7	
gi 22760523 dbj AK074824.1 Homo sapiens cDNA FLJ90343 fis,...	<u>35</u>	2.7	L
gi 30026031 ref NM_178146.1 Mus musculus RIKEN cDNA 181007...	<u>35</u>	2.7	L
gi 26344651 dbj AK075807.1 Mus musculus 10 day old male pa...	<u>35</u>	2.7	L
gi 6650721 gb AF116347.1 AF116347 Homo sapiens SM-11044 bin...	<u>35</u>	2.7	LU
gi 7021041 dbj AK000756.1 Homo sapiens cDNA FLJ20749 fis, ...	<u>35</u>	2.7	LU
gi 17543267 ref NM_067729.1 Caenorhabditis elegans transme...	<u>35</u>	2.7	L
gi 14042725 dbj AK027788.1 Homo sapiens cDNA FLJ14882 fis,...	<u>35</u>	2.7	LU
gi 18088072 gb BC020959.1 BC020959 Homo sapiens, clone MGC:...	<u>35</u>	2.7	LU
gi 9755050 gb AF269150.1 AF269150 Homo sapiens transmembran...	<u>35</u>	2.7	LU
gi 28278504 gb BC046021.1 Danio rerio, Similar to expresse...	<u>35</u>	2.7	
gi 19111161 ref NM_133352.1 Mus musculus RIKEN cDNA 181007...	<u>35</u>	2.7	LU
gi 13435914 gb BC004799.1 Mus musculus RIKEN cDNA 1810073M...	<u>35</u>	2.7	LU
gi 9755052 gb AF269151.1 AF269151 Mus musculus transmembran...	<u>35</u>	2.7	LU
gi 24658498 ref NM_139722.2 Drosophila melanogaster CG1059...	<u>34</u>	3.6	L
gi 17945956 gb AY071401.1 Drosophila melanogaster RE48767 ...	<u>34</u>	3.6	LU

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|9755048|gb|AF269149.1|AF269149 Gallus gallus transmembrane protein TM9SF3 (TM9SF3) mRNA, partial cds
Length = 234

Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +1

Query: 1 DPXFFQHRIVHVSIFN 16
DP FFQHRIVHVSIFN
Sbjct: 112 DPSFFQHRIVHVSIFN 159

☐ >gi|22760523|db|AK074824.1| Homo sapiens cDNA FLJ90343 fis, clone NT2RP2002824, weakly similar to ENDOSOMAL P24A PROTEIN PRECURSOR
Length = 2864

Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +1

Query: 1 DPXFFQHRIVHVSIFN 16
DP FFQHRIVHVSIFN
Sbjct: 145 DPSFFQHRIVHVSIFN 192

☐ >gi|30026031|ref|NM_178146.1| Mus musculus RIKEN cDNA 1810073M23 gene (1810073M23Rik), mRNA
Length = 1155

Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +1

Query: 1 DPXFFQHRIVHVSIFN 16
DP FFQHRIVHVSIFN
Sbjct: 631 DPSFFQHRIVHVSIFN 678

☐ >gi|26344651|db|AK075807.1| Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810073M23 product:unknown EST, full insert sequence
Length = 2479

Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +2

Query: 1 DPXFFQHRIVHVSIFN 16
DP FFQHRIVHVSIFN
Sbjct: 749 DPSFFQHRIVHVSIFN 796

☐ >gi|6650721|gb|AF116347.1|AF116347 Homo sapiens SM-11044 binding protein mRNA, partial cds
Length = 1804

Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +1


Query: 1 DPXFFQHRIVHVSIFN 16
DP FFQHRIVHVSIFN
Sbjct: 604 DPSFFQHRIVHVSIFN 651

☐ >gi|7021041|db|AK000756.1| Homo sapiens cDNA FLJ20749 fis, clone HEP05301
Length = 2973

Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +2


Query: 1 DPXFFQHRIVHVSIFN 16

DP FFQHRH FSIFN
Sbjct: 257 DPSFFQHRHWFSSIFN 304

☐ >gi|17543267|ref|NM_067729.1|  **Caenorhabditis elegans** transmembrane protein TM9SF3 (66.6 kD), mRNA
Length = 1743


Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +1

Query: 1 DPXFFQHRHVFSSIFN 16
DP FFQHRH FSIFN
Sbjct: 610 DPSFFQHRHWFSSIFN 657

☐ >gi|14042725|db|AK027788.1|  **Homo sapiens** cDNA FLJ14882 fis, clone PLACE1003537, weakly similar
to ENDOSOMAL P24A PROTEIN PRECURSOR
Length = 2459


Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +3

Query: 1 DPXFFQHRHVFSSIFN 16
DP FFQHRH FSIFN
Sbjct: 510 DPSFFQHRHWFSSIFN 557

☐ >gi|18088072|gb|BC020959.1|BC020959  **Homo sapiens**, clone MGC:8842 IMAGE:3850015, mRNA, complete cds
Length = 2870

Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +2

Query: 1 DPXFFQHRHVFSSIFN 16
DP FFQHRH FSIFN
Sbjct: 434 DPSFFQHRHWFSSIFN 481

☐ >gi|9755050|gb|AF269150.1|AF269150  **Homo sapiens** transmembrane protein TM9SF3 (TM9SF3) mRNA, complete
cds
Length = 3592


Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +2

Query: 1 DPXFFQHRHVFSSIFN 16
DP FFQHRH FSIFN
Sbjct: 854 DPSFFQHRHWFSSIFN 901

☐ >gi|28278504|gb|BC046021.1| **Danio rerio**, Similar to expressed sequence AW146116, clone
MGC:56246 IMAGE:5601580, mRNA, complete cds
Length = 2082

Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +2


Query: 1 DPXFFQHRHVFSSIFN 16
DP FFQHRH FSIFN
Sbjct: 725 DPSFFQHRHWFSSIFN 772

☐ >gi|19111161|ref|NM_133352.1|  **Mus musculus** RIKEN cDNA 1810073M23 gene (1810073M23Rik), mRNA
Length = 3143

Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +2


Query: 1 DPXFFQHRHVFSSIFN 16
DP FFQHRH FSIFN

Sbjct: 713 DPSFFQHRHHVFSIFN 760

☐ >gi|13435914|gb|BC004799.1|  Mus musculus RIKEN cDNA 1810073M23 gene, mRNA (cDNA clone MGC:8136 IMAGE:3589474), complete cds
Length = 2848


Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +2

Query: 1 DPXFFQHRHHVFSIFN 16
DP FFQHRHH FSIFN
Sbjct: 410 DPSFFQHRHHVFSIFN 457

☐ >gi|9755052|gb|AF269151.1|AF269151  Mus musculus transmembrane protein TM9SF3 (Tm9sf3) mRNA, complete cds
Length = 3143


Score = 34.7 bits (78), Expect = 2.7
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +2

Query: 1 DPXFFQHRHHVFSIFN 16
DP FFQHRHH FSIFN
Sbjct: 713 DPSFFQHRHHVFSIFN 760

☐ >gi|24658498|ref|NM_139722.2|  Drosophila melanogaster CG10590-PA [Drosophila melanogaster] (CG10590) mRNA, complete cds
Length = 2663

Score = 34.3 bits (77), Expect = 3.6
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +1

Query: 1 DPXFFQHRHHVFSIFN 16
DP FFQHRHH FSIFN
Sbjct: 823 DPNFFQHRHHVFSIFN 870

☐ >gi|17945956|gb|AY071401.1|  Drosophila melanogaster RE48767 full length cDNA
Length = 2662

Score = 34.3 bits (77), Expect = 3.6
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +1

Query: 1 DPXFFQHRHHVFSIFN 16
DP FFQHRHH FSIFN
Sbjct: 823 DPNFFQHRHHVFSIFN 870

Get selected sequences

Select all

Deselect all

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,
or phase 0, 1 or 2 HTGS sequences)

Posted date: May 30, 2003 12:03 AM

Number of letters in database: -276,428,487

Number of sequences in database: 1,772,460

Lambda	K	H
0.345	0.155	0.557

Gapped		
Lambda	K	H
0.267	0.0410	0.140

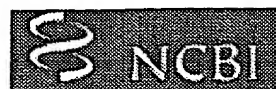
Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 186,634,521

Number of Sequences: 1772460

Number of extensions: 713471
Number of successful extensions: 33235
Number of sequences better than 10.0: 16
Number of HSP's better than 10.0 without gapping: 29804
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 33235
length of query: 17
length of database: 2,771,168,700
effective HSP length: 0
effective length of query: 24
effective length of database: 2,771,168,700
effective search space: 66508048800
effective search space used: 66508048800
frameshift window, decay const: 50, 0.1
T: 13
A: 40
X1: 15 (7.5 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 38 (21.6 bits)
S2: 73 (32.7 bits)



NCBI Nucleotide

Search for

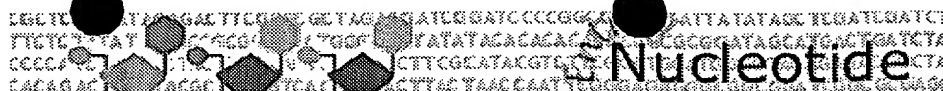
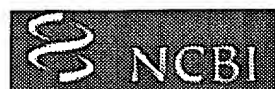
Display Limits Show: Preview/Index History Clipboard

☐ 1: AF269149. Gallus gallus tra...[gi:9755048]

LOCUS AF269149 234 bp mRNA linear VRT 09-AUG-2000
DEFINITION Gallus gallus transmembrane protein TM9SF3 (TM9SF3) mRNA, partial cds.
ACCESSION AF269149
VERSION AF269149.1 GI:9755048
KEYWORDS
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 234)
AUTHORS Gong, T. W., Hegeman, A. D., Shin, J. J., Adler, H. J., Raphael, Y. and Lomax, M. I.
TITLE Identification of genes expressed after noise exposure in the chick basilar papilla
JOURNAL Hear. Res. 96 (1-2), 20-32 (1996)
MEDLINE 96414275
PUBMED 8817303
REFERENCE 2 (bases 1 to 234)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Evolution of the TM9 Super Family of Membrane Spanning Proteins
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 234)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2000) Kresge Hearing Research Institute, University of Michigan, 9301E MSRB III, 1150 West Medical Center Drive, Ann Arbor, MI 48109-0648, USA
FEATURES
source Location/Qualifiers
1..234
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/tissue_type="basilar papilla"
gene <1..>234
/gene="TM9SF3"
CDS <1..>234
/gene="TM9SF3"
/note="transmembrane protein 9 superfamily member 3"
/codon_start=1
/product="transmembrane protein TM9SF3"
/protein_id="AAF98158.1"
/db_xref="GI:9755049"
/translation="ASEGKVKLVPTNKIQMSYSMKWKSDVKFEDRFDKYLDPSPFFQHRIHWFSIFNSFMMVIFLVGLVSMILMRTLRLKKKK"
BASE COUNT 80 a 38 c 46 g 70 t
ORIGIN
1 gccagcgaag gaaagtgaa actggtacca aatacaaaaa tccagatgtc atatttatg
61 aagtgaaga agtcagatgt gaaattgaa gaccgatttg acaagtacct tgacctatc
121 ttctttcagc acagaattca ctggttttca attttcaatt ctttcagat ggtgatctt
181 ctggttgcc tagtgtctat gatattaatg agaactttgc gaaaaaaaa aaaa
//

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

May 20 2003 11:20:11



PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Books

Search for

Limits

Preview/Index

History

Clipboard

Details

Display Show: ☐ 1: NM_178146. Mus musculus RIKE...[gi:30026031]

Links

LOCUS 1810073M23Rik 1155 bp mRNA linear ROD 18-MAY-2003

DEFINITION Mus musculus RIKEN cDNA 1810073M23 gene (1810073M23Rik), mRNA.

ACCESSION NM_178146

VERSION NM_178146.1 GI:30026031

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1155)

REFERENCE

AUTHORS

Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L., Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J., McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S., Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalón, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 1155)

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusica, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

REFERENCE 3

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from AK075807.1.

FEATURES
Location/Qualifiers
source 1..1155
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="19"
gene 1..1155
/gene="1810073M23Rik"
/note="synonyms: SMBP, Tm9sf3, 2810031D16Rik"
/db_xref="LocusID:107358"
/db_xref="MGI:1914262"
CDS 1..1155
/gene="1810073M23Rik"
/note="putativeunknown EST (GB|BG073434, evidence: BLASTN,
99%, match=803); SM-11044 binding protein"
/codon_start=1
/product="transmembrane protein 9 superfamily member 3"
/protein_id="NP_835359.1"
/db_xref="GI:30026032"
/db_xref="LocusID:107358"
/db_xref="MGI:1914262"
/translation="MRPLPGAPGVAAAAALLLLLPRARSDEHEHTYQDKEEVVLWMN
TVGPYHNROETKYFSLPFCVSGSKSISHYHETLGEALQGVLEFSGLDIKFKDDVMP
GTyceIDLDKEKRDAFVYAIKNHYWYQNYIDDLPIWGIWGEADENGEDYYLWYKYLE
IGFNGNRIVDVNLTEGKVKLVPTKIQMSYSVKWKKSDVKFEDRFDKYLDPSFFQHR
IHWFSIFNSFMVIFLVGLVSMILMRTLKDYARYSKEEEMDDMDRLGDEYGWKQVH
GDVFRPSSHPLIFSSLIGSGCQIFAVSLIVIIAMIEDLYTERGSMLSTAFVYAATS
PVNGYFGGSLYAROGGRRWIKDYYRGIPYPSYGVWHCILHQLYSHLLPCL"
misc_feature 160..1071
/gene="1810073M23Rik"
/note="EMP70: Region: Endomembrane protein 70"
/db_xref="CDD:pfam02990"

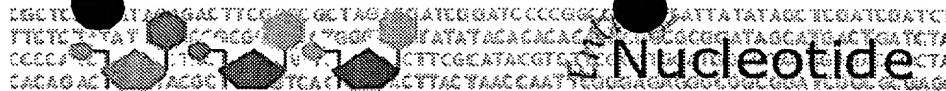
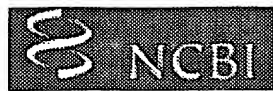
BASE COUNT 340 a 199 c 278 g 338 t
ORIGIN

```
1 atgaggccgc tgcggggcgc tctggcgtg gggggggcgc ccgcgttgtt gttgctgctg
61 ctgccccggg ctcggtctga cgagcacgaa cacacgtatc aagataaaga agaagttgtt
121 ttatggatga atactgttgg gccctaccac aatcgccaag aaacataaa atacttttca
181 cttccattct gtgtggggtc aaaaaaaagt atcagtcatt accatgaaac ttggggagaa
241 gcacttcaag gaggttgaatt agaatttagt ggcctggaca ttaaatttaa agatgatgtg
301 atgccaggca cttactgtga aattgactta gataaagaga agagagatgc gtttgtgtat
361 gctatcaaga atcactattg gtatcagatg tacatagatg acttaccat atgggggtatt
421 gttggtgaag cagatgaaaa tggggaagat tactatcttt gacactacaa aaaacttgaa
481 ataggcttta atggaaatcg aattgttgat gttaatctaa ctagtgaagg aaaggtcaag
541 ctggttccaa atactaaaat acagatgtca tattcggtaa aatggaaaaa atcggatgta
601 aaatttgaag atcgatttga taaatatott gatccatcct ttttcagca taggattcac
661 tggttttcaa tttttaattc cttcatgatg gtgatcttct tagtgggatt agtttcaatg
721 attttaatga gaactttaag gaaagattat gcccgataca gtaaagaaga agaatggat
781 gacatggaca gagacctagg agacagtat ggctggaagc aggtgcatgg agatgtgttc
841 agaccgtcaa gtcacctctc gatcttctcc tccctcattg gctctggatg tcagatattt
901 gctgtgtctc tcattgttat tattgttgcc atgatatagg acttatatac agagaggggg
961 tcaatgctca gcacagccat atttgtctat gctgctacat cgccagtga cgggtacttt
1021 ggagggaagtc tgtatgctag acaaggagga aggagatgga taaaggatgt ttatcggggc
1081 attcattatc ccagctatgg tgtgtggcac tgcattcttc atcaacttta tagccattta
1141 ttaccatgcc tctag
```

//

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

May 20 2003 11:20:11



Search for

Display Show:

Limits Preview/Index History Clipboard Details

☐ 1: AF116347. Homo sapiens SM-1...[gi:6650721]

LOCUS AF116347 1804 bp mRNA linear PRI 16-OCT-2001
DEFINITION Homo sapiens SM-11044 binding protein mRNA, partial cds.
ACCESSION AF116347
VERSION AF116347.1 GI:6650721
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
REFERENCE 1 (bases 1 to 1804)
AUTHORS Sugawara, T., Lenzen, G., Simon, S., Hidaka, J., Cahen, A.,
Guillaume, J. L., Camoin, L., Strosberg, A. D. and Nahmias, C.
TITLE The iodocyanopindolol and SM-11044 binding protein belongs to the
TM9SF multispinning membrane protein superfamily
JOURNAL Gene 273 (2), 227-237 (2001)
MEDLINE 21479397
PUBMED 11595169
REFERENCE 2 (bases 1 to 1804)
AUTHORS Sugawara, T., Lenzen, G., Simon, S., Hidaka, J., Cahen, A.,
Guillaume, J. L., Camoin, L., Nahmias, C. and Strosberg, A. D.
TITLE Direct Submission
JOURNAL Submitted (23-DEC-1998) Vetigen, 21 rue Sebastien Mercier, Paris
75015, France
FEATURES
source Location/Qualifiers
1..1804
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="skeletal muscle"
CDS
1..1737
/note="contains nine potential membrane spanning domains;
similar to yeast EMP70 protein precursor encoded by
GenBank Accession Numbers X67316 and S25110"
/codon_start=1
/product="SM-11044 binding protein"
/protein_id="AAF21983.1"
/db_xref="GI:6650722"
/translation="AAAALWLLLLPRTRADEHEHTYQDKEEVLMNNTVGPYHNRO
ETKYFSLPFCVSGSKSISHYHETLGEALQVLEFSGLDIKFKDDVMPATYCEIDLD
KEKRDAFVYAIKNHYWYQMYIDDLPIWGIVGEADENGEDYLLWYKLEIGFNGNRIV
DVNLTSEGVKVLVPNTKIQMSYSVKWKKSDVKFEDRFDKYLDPSPFFQHRHWFHSIFNS
FMVNLFLVGLVSMILMRTLKDYARYSKEEEMDDMDRLGDYEGWKQVHGDVFRPSSH
PLIFSSLIGSGCQIFAVSLIVIIIVAMIEDLYTERGSMLSTAFVYAATSPVNGYFGGS
LYARQGGRRWIKOMFIGAFLIPAMVCGTAFFINFIAIYYHASRAIPFGTMVAVCCICF
FVILPLNLVGTILGRNLGQPNFPCRVNAVPRPIPEKKWFMEPAVIVCLGGILPFGSI
FIEMYIFTFSWAYKIIYYVYGFMMVLVLILCIVTVCVTIVCTYLLNAEDYRWQWTSF
LSAASTAIYYMYSFYYYFFKTKMYGLFQTSFYFGYMAVFSTALGIMCGAIGYMGTS
A
FVRKIYTNVKID"

BASE COUNT 509 a 301 c 403 g 591 t
ORIGIN

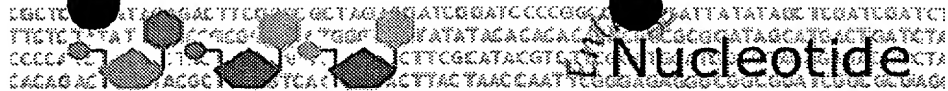
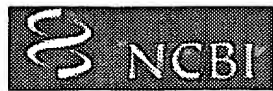
```
1 gggcgccg cgtgtgct gctgtgctg ctgtgccc ggaccgggc ggacgagcac
61 gaacacacgt atcaagataa agaggaaatt gtcttatgga tgaatactgt tgggccctac
121 cataatcgtc aagaacataa taagtacttt tcatttccat tctgtgtggg gtcaaaaaaa
181 agtatcagtc attaccatga aactctggga gaagcacttc aagggttga attggaattt
241 agtggctctg atattaaatt taaagatgat gtgatgccag ccacttactg tgaattgat
301 ttgataaag aaaagagaga tgcatttcta tatgccataa aaatcatta ctgtaccag
361 atgtacatag atgatttacc aatatgggt attgtggtg agcgtgatga aaatggagaa
421 gattactatc ttggacctt taaaaaactt gaaatagggt ttaattgaaa tcgaattgtt
481 gatgttaatc taactagtga aggaaggtg aaactggttc caaatactaa aatccagatg
541 tcatttcag taaaatggaa aaagtcagat gtgaaattg aagatcgatt tgacaaatat
601 ctgtatccgt ccttttttca acatcggatt cattggtttt caattttcaa ctcttcattg
661 atggtgatct tctgtgtggg cttagtttca atgattttta tgagaacatt aagaaaagat
721 tatgtcgggt acagttaaga ggaagaaatg gatgatattg atagagacct aggagatgaa
781 tatggatgga aacagtgcca tggagatgta tttagaccat caagtcaccc actgatattt
841 tctctctgta ttggtctggt atgtcagata tttgtgtgt ctctcatcgt tattattgtt
901 gcaatgatag aagatttata tactgagagg ggaatcaatg tcagtacagc catatttgc
961 tatgtgcta cgtctccagt gaattggtat tttggaggaa gtctgtatgc tagacaagga
1021 ggaaggagat ggataaagca gatgtttatt gggcatttcc ttatccagc tatggtgtgt
1081 ggcactgcc tcttcatcaa ttcatagcc atttattacc atgcttcaag agccattcct
1141 ttggaacaa tgggtggcgt ttgttcacg tgtttttttg ttattcttcc totaaatcct
1201 gttgtgtaaa tacttggcgg aaatctgtca ggtcagccca actttcctt tcgtgtcaat
```

1261 gctgtgcctc gtcctatacc ggagaa tggttcatgg agcctgcggt tattgtttgc
1321 ctgggtggaa ttttaccttt tggttcaatc tttattgaaa tgtatttcat cttcacgtct
1381 ttctgggcat ataagatcta ttatgtctat ggcttcatga tgcgtgtgct ggttatcctg
1441 tgcattgtga ctgtctgtgt gactattgtg tgcacatatt ttctactaaa tgcagaagat
1501 taccgggtggc aatggacaag ttttctctct gctgcatcaa ctgcaatcta tgtttacctg
1561 tattcctttt actactattt ttcaaaaaca aagatgtatg gcttatttca aacatcattt
1621 tactttggat atatggcggg attttagcaca gccttgggga taatgtgtgg agcgattggt
1681 tacatgggaa caagtgcctt gtccgaaaa atctatacta atgtgaaaat tgactagaga
1741 cccaagaaaa cctggaactt tggatcaatt tcttttcat aggggtggaa cttgcacagc
1801 aaaa

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

May 20 2003 11:20:12



Search for

Display Show:

Links

1: NM_067729. Caenorhabditis el...[gi:17543267]

LOCUS 4C515 1743 bp mRNA linear INV 22-NOV-2002
DEFINITION Caenorhabditis elegans transmembrane protein TM9SF3 (66.6 kD), mRNA.
ACCESSION NM_067729
VERSION NM_067729.1 GI:17543267
KEYWORDS
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
COMMENT VALIDATED REFSEQ: This record has undergone preliminary review of the sequence, but has not yet been subject to final NCBI review. The reference sequence was derived from WormBase CDS:Y41D4A.4. Fully supported by cDNA from the Worm Transcriptome Project. COMPLETENESS: full length.
FEATURES
source Location/Qualifiers
1..1743
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/db_xref="taxon:6239"
/chromosome="IV"
/map="IV:-15.38 cM (interpolated genetic position)"
/map="IV: covering 5823 bp, from base 1745879 to 1751703 on genome release WS85"
/clone="Primers to amplify the CDS (Stop included): ATCGGGTACTGATAAGCC (T=57.6). TTAATCGATTTTACAGTCTGATAGATT (T=56.4)"
/clone_lib="[Predicted cellular localisation] PSORT II analysis. (K. Nakai) trained on yeast data predicts that the subcellular location of this protein is most likely in the endoplasmic reticulum (66%) or in the plasma membrane (33%)."
gene 1..1743
/gene="4C515"
/locus_tag="4C515"
/note="synonyms: Y41D4A.4, CELK01378"
CDS 1..1743
/gene="4C515"
/locus_tag="4C515"
/function="Transporter GO:0005215 [Pfam/Interpro/GO]"
/function="Transport GO:0006810 [Pfam/Interpro/GO]"
/function="Integral membrane protein GO:0016021 [Pfam/Interpro/GO]"
/note="|| [Common ancestor, from TaxBlast with threshold 10-3] Eukaryota || [Closest homologs] Dictyostelium discoideum: emb|CAC47950.1| (score=271); Arabidopsis thaliana: ref|NP_563881.1| (528); Saccharomyces cerevisiae: ref|NP_010392.1| (211); Schizosaccharomyces pombe: ref|NP_596464.1| (177); Caenorhabditis elegans: ref|NP_500130.1| (1028); Anopheles gambiae str PEST: gb|EAA09712.1| (724); Drosophila melanogaster: ref|NP_647979.1| (728); Mus musculus: ref|NP_579930.1| (760); Homo sapiens: ref|XP_050993.1| (761)"
/codon_start=1
/product="Transmembrane protein TM9SF3 (66.6 kD)"
/protein_id="NP_500130.1"
/db_xref="GI:17543268"
/db_xref="AceView/WormGenes:4C515"
/db_xref="CDD:pam02990"
/db_xref="LocusID:176983"
/db_xref="NextDB:CELK01378"
/db_xref="WormBase:Y41D4A.4"
/translation="MRVLSLLFTSLLVEADEHDLHYEVEEVVLMNTVGPYSNRO ETTYFSLPFCCKGKKEIGHYHETMGESLLGVELEFSGLDIKFRNTNKKTVVCEKKLT ETDYKTLLEYAIONSYYYQMYLDDMPWGMVGEIDNTVNPAYKLYTHKRLDIGYNDQ VVDVNLTTDGRVDIRPGAELTFYEVQWSKSEVDFTKRFDKLYDPSFFQHR|HWFIF NSFMMVFLVGLVWMLVRLTLRKDYARYOKEDSLDDLDLDEYGWKQVHGDVFRPP SMLPLFSSCIGAGYHVFTVAITTLAIVGEFYTERGSLLSAAIFVYAACSPVNGYAG GSYARFGGRHWIKOMLLGAFLPSMVCVAFINFIAYYHASRAIPFTIMLAVSAI CLFVILPLTLVGTVIGRNAGSADYPCRVNAVPRIPDKKWFVQVWILTAGGVLPFG SIFIEYFIFTSFWAYKIYVYGFMLLVITILSIVTVCVTVCSYFLNLAEDYRWRWT"

SFACGASTAFVYMYMYS FKTKMYGLFQTVFYFGYMGIFAALGLMTGTIGYVGT
 AKFVRKIYQTVKID~
misc feature 1..51
 / gene="4C515"
 / locus_tag="4C515"
 / note="Region: [PSORT] N terminal signal domain"
misc feature 133..1614
 / gene="4C515"
 / locus_tag="4C515"
 / note="Region: [Pfam/InterPro description] endomembrane
 protein 70: the transmembrane 9 superfamily protein
 (TM9SF) may function as a channel or small molecule
 transporter. Proteins in this group are endosomal integral
 membrane proteins. HMMER score 820.10 Eval=5.1e-244"
 / db_xref="CDD:pfam02990"
misc feature 658..708
 / gene="4C515"
 / locus_tag="4C515"
 / note="Region: [PSORT] transmembrane domain:
 SFMMVVFLVGLVWMILV"
misc feature 874..924
 / gene="4C515"
 / locus_tag="4C515"
 / note="Region: [PSORT] transmembrane domain:
 VFTVAVITTLAIVGEF"
misc feature 937..987
 / gene="4C515"
 / locus_tag="4C515"
 / note="Region: [PSORT] transmembrane domain:
 GSLLSAAIFVYAACSPV"
misc feature 1054..1104
 / gene="4C515"
 / locus_tag="4C515"
 / note="Region: [PSORT] transmembrane domain:
 LGAFLLPSMVCVAFLLI"
misc feature 1159..1209
 / gene="4C515"
 / locus_tag="4C515"
 / note="Region: [PSORT] transmembrane domain:
 LAVSAICLFVILPLTLV"
misc feature 1312..1362
 / gene="4C515"
 / locus_tag="4C515"
 / note="Region: [PSORT] transmembrane domain:
 WLITLAGGVLPFGSIFI"
misc feature 1426..1476
 / gene="4C515"
 / locus_tag="4C515"
 / note="Region: [PSORT] transmembrane domain:
 LLVTIILSIVTVCVTIV"
misc feature 1726..1737
 / gene="4C515"
 / locus_tag="4C515"
 / note="Region: [PSORT] ER membrane domain: TVKI~

BASE COUNT 442 a 428 c 404 g 469 t
 ORIGIN

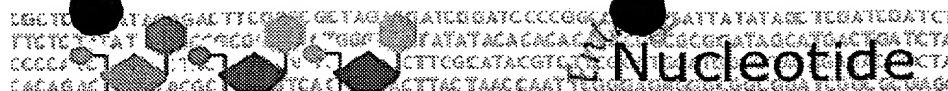
```

1 atcggggtac tgataagcct gctactatct acctcgctgc tcgtcgaagc cgacgaacac
61 gaccatttgt acgaggtctc cgaggagggt gtattatgga tgaacacggt gggaccctac
121 tcgaatcgcc aggaaaccta caccactctc tccctgccat ttgttaaagg agagaagaag
181 gaaattggcc attatcacga aactatggga gaatactgc tcggcgtgga gctagagttc
241 tccggattgg atataaaatt cagaacaac accaagaaaa ccgtgggttg cgagaagaag
301 ctacccgaaa ccgactataa aacgctgctc tacgctatcc aaaacagcta ttactatcaa
361 atgtacctgc acgacatgcc gatttgggga atggttgagg aaatcgataa tactgtgaat
421 ccgccggcct acaagcttta tacgcataag aggctagata ttggctataa cgataagcag
481 gtggtcgacg tgaatttgac aacagacgga agagttgata ttgcgtccgg cgctgagctc
541 acgttcacct atgaggtgca atggagcaag tcggaagtgg attttaccaa gagattcgat
601 aaatatctcg atccaagctt ctccagcac agaatccact ggttctcgat ttttaacagt
661 ttcattgatg tcgtattcct cgtcggattg gtatggatga ttctagtccg tactctacga
721 aaagactacg ccgactacga aaaagaggat agtctcgacg atttggacgc cgtactcgga
781 gatgagtacg gttggaacaa ggttcacgga gacgtcttcc gtccaccatc aatgccgttg
841 ctcttctcat cgtgtattgg agccgggtat catgtgttca ctgtcgcggt tattacgacg
901 attttggcga ttgttgaga attttataca gaacggcgtt ccctactctc cgcgcgaatc
961 ttgctctacg ccgcttgctc gccagtcaac ggaatgccc gggatcgat gtaogccaga
1021 ttcggaggtc gtacattgat caagcaaatg ctctcggag cattccttct gccaaagtatg
1081 gtgtgtgtgt tcgcattcct tatcaacttt atcgcgatct actatcacgc gtcacgcgcc
1141 attccattca caattatgct cgcgtctcgc gcgatctgco tctttgtgat ccttccgctg
1201 actcttgtcg gaactgtgat cggaagaagt atggctggaa gtgcagacta tccgtgtaga
1261 gtgaatgccg tgcgcgagac cattcctgat aagaaatggt tcgtccaacc gtgctcatc
1321 acccttgccg gaggtgttct cccattcgga tccatcttca tcgaatgta tttatcttc
1381 accctattct gggcgtacaa aatctattat gtgtacggat tcatgtttt ggtcacaaata
1441 atcctgtcaa ttgtcacctg atgcgtcaca attgtctgct cctacttctc actcaacgcc
1501 gaggattata gatggagatg gacgagcttc cgtgtggagg catctactgc attctatgtg
1561 tacatgtatt ccatgtatta ttcttcttcc aagacaaaaa tgtacggact ttcccaaacg
1621 gtcttctact ttggatacat gggaatcttc gccgccgctc tcggactcat gaccggcacc
1681 atcggatacg tcggaaccgc caaatctgct cgcgaatct atcagactgt gaaaatcgat
1741 taa
  
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

May 20 2003 11:20:12



Search for

Display Show:

History Clipboard Details

☐ 1: AF269150. Homo sapiens tran...[gi:9755050]

LOCUS AF269150 3592 bp mRNA linear PRI 09-AUG-2000
DEFINITION Homo sapiens transmembrane protein TM9SF3 (TM9SF3) mRNA, complete cds.
ACCESSION AF269150
VERSION AF269150.1 GI:9755050
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3592)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Evolution of the TM9 Super Family of Membrane Spanning Proteins
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3592)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2000) Kresge Hearing Research Institute, University of Michigan, 9301E MSRB III, 1150 West Medical Center Drive, Ann Arbor, MI 48109-0648, USA

FEATURES
source
1..3592
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="10"
/map="10q23-q24"
gene
1..3592
/gene="TM9SF3"
CDS
218..1987
/gene="TM9SF3"
/note="transmembrane protein 9 superfamily member 3"
/codon_start=1
/product="transmembrane protein TM9SF3"
/protein_id="AAF98159.1"
/db_xref="GI:9755051"
/translation="MRPLPGALGVAAAAALWLLLLLPRTRADEHEHTYQDKEEVVLV
MNTVGPYHNRQETKYFSLPFCVGSKKSI SHYHETLGEALQGVLEFSGLDIKFKDDV
MPATYCEIDLDEKRDFAFYAIKNHYWYQYIDDLPIWGI VGEADENGEDYYLWYTK
LEIGFNGNRIVDVNLTSSEKVKLVNPKIQISYSVKWKSDVKFEDRFDKYLDPSFFQ
HRIHWFSIFNSFMMVIFLVGLVSMILMRTLKDYARYSKEEEMDDMDRLDGEYGWKQ
VHGDVFRPSSHPLIFSSLIGSGCQIFAVSLVIVAMIEDLYTERGSMLSAIFVYAA
TSPVNGYFGSLYAROGGRRWIKQMFIGAFLIPAMVCGTAFFINFIAIYYHASRAIP
GTMVAVCCICFFVILPLNLVGTILGRNLSGQPNFCRVNAVPRPIPEKKWFMPEAVIV
CLGGILPFGSIFILEMYFIFTSFWAYKIYVYVGFMMVLVLICIVTVCVTVCTYFLLN
AEDYRWQWTSFLSAASTAIYVYMYSFYFFYFKTKMYGLFQTSFYFGYMAVFSTALGIM
CGAIGYMGTSFAVRKIYTNVKID"

BASE COUNT 1026 a 604 c 815 g 1147 t
ORIGIN

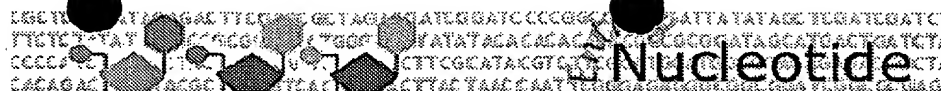
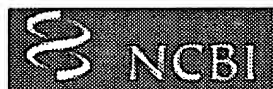
```
1 gaggaagagg ctgaggaggc gceggggcgc ggggaggctc aggaagcggc ggtgacggcg
61 acggcgcgcg cagaggaggc agcggtctgg cggggccccc tgcgtctgtc cggcccccgt
121 ggatgcgaat cggccgcggc ggaggcggcg cggcgaggag aggcggcgccg gggaggagga
181 gtcggtgagc cggctcggcg cgggaggggc cgggaggatg aggcggctgc ctggcgctct
241 tggcgtggcg cggcgccggc cgtctggctg gctgctgctg ctgctgcccc ggaccggggc
301 ggacgagcac gaacacacgt atcaagataa agaggaaagt gtcttatgga tgaatactgt
361 tggggccctac cataatcgct aagaacataa taagtacttt tcaactccat tctgtgtggg
421 gtcaaaaaaa agtatcagtc attaccatga aactctggga gaagcacttc aagggttga
481 attggaattt agtggtctgg atattaaatt taaagatgat gtgatgccag ccacttactg
541 tgaaattgat ttagataaag aaaagagaga tgcatttgta tatgccataa aaaatcatta
601 ctggtaccag atgtacatag atgatttacc aatatggggt attgttggtg aggcgtgatga
661 aaatggagaa gattactatc ttggacctta taaaaaacct gaaatagggt ttaatggaaa
721 tcgaattggt gatgttaatc taactagtga aggaagggtg aaactgggtc caaatactaa
781 aatccagatt tcatattcag taaaatggaa aaagtcagat gtgaaatttg aagatcgatt
841 tgacaaatat cttgatccgt ctttttttca acatcggatt cattggtttt caattttcaa
901 ctcttctcatg atgtgatctt tcttggtggg cttagtttca atgattttaa tgagaacatt
961 aagaaaagat tatgctcggt acagtaaaga ggaagaaatg gatgatattg atagagacct
1021 aggagatgaa tatggatgga aacagggtgca tggagatgta tttagaccat caagtacccc
1081 actgatattt tctctctgta ttggttctgg atgtcagata tttgctgtgt ctctcatcgt
1141 tattattggt gcaatgatag aagatttata tactgagagg ggaatcaatgc tcaatcagac
1201 catatttgct tatgctgcta cgtctccagt gaatggttat ttggaggaa gtctgtatgc
1261 tagacaagga ggaaggagat ggataagca gatgtttatt gggcatttcc ttatccagc
```

1321 tatggtgtgt ggcactgcct tottca tttcatagcc atttattacc atgcttcaag
1381 agccattcct tttggaacaa tgggtgccgt ttgttgcac tggttttttg ttattcttcc
1441 tctaaatcct gttggtacaa tacttgccg aaatctgtca ggtcagccca actttccttg
1501 tegtgtcaat gctgtgcctc gtctatatac ggagaaaaaa tggttcatgg agcctgcggt
1561 tattgtttgc ctgggtggaa ttttaccttt tggttcaatc tttattgaaa tgtatttcat
1621 ctccacgtct ttctgggcat ataagatcta ttatgtctat ggcttcatga tgcgtgtgct
1681 ggttatcctg tgcatttga ctgtctgtgt gactattgtg tgcacatatt ttctactaaa
1741 tgcagaagat taccggtggc aatggacaag tttctctctc gctgcatcaa ctgcaatcta
1801 tgtttacatg tattcctttt actactattt tttcaaaaca aagatgtatg gcttatttca
1861 aacatcattt tacttttggat atatggcggg atttagcaca gccttgggga taatgtgtgg
1921 agcgattggg tacatgggaa caagtgcctt tgtccgaaaa atctatacta atgtgaaaat
1981 tgactagaga cccaagaaaa cctggaactt tggatcaatt tctttttcat aggggtggaa
2041 ctgacacagc aaaaacaaac aaacgcaaga agagatttgg gctttaacac actgggtact
2101 ttgtgggtct ccttttgcgc ggtggcttaa agtaacatct atttccattg atcctaggtt
2161 ctctcgtact gctttctcca actgttcaca gcaaatgctt ggattttatg cagtaggcac
2221 tactacagta catggctaata ctcccaaaaa actagctcat taaagatgaa atagaccagc
2281 tctcttcagt gaagaggaca aatagtttat ttaaagcatt tgtccaata aaataaatag
2341 agggaaactt ggatgctaaa attacatgaa taggaatctt cctggcactt agtgtttcta
2401 tgttattgaa aaatgatgtt ccagaaagat tacttttttc ctcttatttt tactgccatt
2461 gtcagacctat tgtgggacat ttttatatat tgaatctggg ttcttttttg actttttttt
2521 ttcccaatcc aacagcatcc ttttttttaa aagagagaat tagaaaaat taaatcctgc
2581 atgtaataata tctgctgtca tottagttgg accaacttcc catttattta tottaaaact
2641 atacagttaac atcttaattc catccaaaga agatacagtt tgaagacaga agtgactctt
2701 ctacaatgca atttactgta cagttagaaa gcaaaagtgtt aaatggagaa gatacttgtt
2761 tttattaaac attttgagat ttagataaac tacattttta ctgaatgtct aaagtatta
2821 tcttttttcc ccccaagtta gtcttaaatc ttttgggttt gaatgaaggt tttacataag
2881 aaattattaa aaacaagggg ggtgggtaat aaatgtatat aacattaaat aatgtaacgt
2941 aggtgtagat tcccaaatgc atttggatgt acagatcgac tacagagtac tttttcttta
3001 tgaatgattg ttagaaaatg tgtgatttgg gtgggctttt acatcttgcc taccattgca
3061 tgaacacattg ggttttcttc aaaatgtgtg tgtcactact cttttgggag gggggttgtt
3121 ttcttctgtt tattttctga gactcctaca ggagccaaat ttgtaattta gagacactta
3181 attttgttaa tctgtctgtg gacacttaag taacatctaa agcattattg ctttagaatg
3241 ttcaaaataa atttcctgac caaattgttt tgtggaaata gatgtgtttg caatttgaag
3301 atatctttct gtccagaagg caaaattacc gaatgccatt tttaaaagta tgcataaac
3361 tatgtctact tcatacaggg gacccgtatt ttaaaatctc cagacttgct tacatctaga
3421 ttatccagca caatcataaa gtgaatgaca aacctttga atgaaattgt ggcacaaaaa
3481 ctgttcagggt tgggtaccg tgtaaagtgg ggtgggggta aaagtgtta acgtactgtt
3541 ggatcaacaa ataaagggtta cagttttgta agagaaaaaa aaaaaaaaaa aa

//

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

May 20 2003 11:20:11



Search for

Display Show:

☐ 1: AF269151. Mus musculus tran...[gi:9755052]

LOCUS AF269151 3143 bp mRNA linear ROD 09-AUG-2000
DEFINITION Mus musculus transmembrane protein TM9SF3 (Tm9sf3) mRNA, complete cds.
ACCESSION AF269151
VERSION AF269151.1 GI:9755052
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3143)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Evolution of the TM9 Super Family of Membrane Spanning Proteins
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3143)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2000) Kresge Hearing Research Institute, University of Michigan, 9301E MSRB III, 1150 West Medical Center Drive, Ann Arbor, MI 48109-0648, USA

FEATURES
source Location/Qualifiers
1..3143
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
gene 1..3143
/gene="Tm9sf3"
CDS 83..1846
/gene="Tm9sf3"
/note="transmembrane protein 9 superfamily member 3"
/codon_start=1
/product="transmembrane protein TM9SF3"
/protein_id="AAF98160.1"
/db_xref="GI:9755053"
/translation="MRPLPGAPGVAAAAALLLLLPRARSDEHEHTYQDKEEVVLWMN TVGPYHNRQETKYFSLPFCVSGSKSISHYHETLGEALQGVLEFSGLDIKFKDDVMP GTYCEIDLDEKRDADFVYAIKNHYWYQMYIDLP IWGIVGEADENGEDYYLWYKKLE IGFGNGRIQDVNLTSEGKVKLVPTNKIQMSYSVKWKKSDVKFEDRFDKYLDPSFFQHR IHWFSIFNSFMVMVIFLVGLVSMILMRTLKRDYARYSKEEEMDDMDRLGDYEWKQVH GDVFRPSSHPLIFSSLIGSGCQIFAVSLIVIIAMIEDLYTERGSMSTAIIFYAATS PVNGYFGGSLYAROGGRRWIKOMFIGAFLIPAMVCGTAFFINFIAIYYHASRAIPFGT MVAVCCICFFVILPLNLVGTILGRNLGQPNFPCRVNAVPRPIPEKKWFMEPAVIVCL GGILPFGSIFIEYMFIFTSFWAYKIIYYVGFMMMLVLVILCIVTVCVTVCTYFLLNAE DYRWQWTSFLSAASTAIYYMYSFYYFFKTKMYGLFQTSFYFGYMAVFSTALGIMCG AIGYMGTSAFVRKIYTNVKID"

BASE COUNT 868 a 564 c 699 g 1012 t
ORIGIN

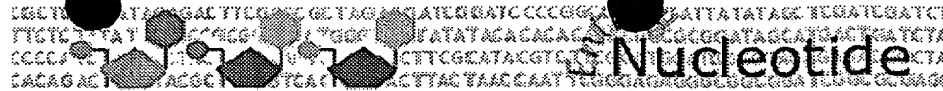
```
1 tccgcgcgcc gttgatgtga atcgcgcgcg ggcgcgcgagg agggatcggt ggcgcgcgcg
61 ccgcgcgtgt ggcgcgcgga ggcgcgcgcg ggcgcgcgcg ggcgcgcgcg ggcgcgcgcg
121 ccgcgcgtgt ggcgcgcgga ggcgcgcgcg ggcgcgcgcg ggcgcgcgcg ggcgcgcgcg
181 tcaagataaa gaagaagtgt ttttatggat gaatactgtt ggcgcgcgcg acaatcgcca
241 agaaacatat aaatactttt cacttcattt ctgtgtgggg tcaaaaaaaa gtatcagtca
301 ttaccatgaa actttgggag aagcacttca aggcattgaa ttgaatttta gtgccttgga
361 cattaaattt aaagatgatg tgatgccagg cacttactgt gaaattgact tagataaaga
421 gaagagagat gcgtttgtgt atgctatcaa gaatcactat tggatcaga tgtacataga
481 tgacttacca atatggggtt ttgttggtga agcagatgaa aatggggaag attactatct
541 ttggacctac aaaaaacttg aaataggctt taatggaaat cgaattgttg atgttaactt
601 aactagttaa ggaagggtca agctggttcc aaatactaaa atacagatgt catattcggt
661 aaaaatgaaa aaatcggtat taaaatttga agatcgattc gataaatatc ttgatccatc
721 cttttttcag cataggattc actggttttc aatttttaat tccttcata tggatgatctt
781 cttagtggga ttagtttcaa tgatttttaat gagaacttta aggaagattt atgcccagata
841 cagtaaagaa gaagaaatgg atgacatgga cagagacctt ggagacaggt atggctggaa
901 cgaggtgcgt ggagatgtgt tcagaccgtc aagtcaccct ctgatcttct cctccctcat
961 tggctctgga tgcagatat ttgtgtgttc tctcattgtt attattgttg ccatgataga
1021 ggaattatat acagagaggg ggtcaatgct cagcacagcc atatttgtot atgtgtotac
1081 atcgcgcagt aacgggtact ttggaggaag tctgtatgct agacaaggag gaaggagatg
1141 gataaagcag atgtttatcg ggcatttctt tatccagctt atggtgtgtg gcaatgcatt
1201 cttcatcaac ttatagcca ttatttacc tgcctctaga gccatttctt ttggaacaat
1261 ggtggcgtgt ttgtgcatct gttttttgt tatccttctt ctaaatctcg ttgttacaat
1321 actgggtcga aatgtgtcgg gtcagcccaa cttcccttgt cgtgtcaatg ccgtgcctcg
1381 tccatcccg gaaaaaaat ggtttatgga gctgcagtt attgtttgcc tgggaggaat
```

1441 tttacctttt ggatcaatct ttattt gttacttcato ttcacgtcct tctgggcata
1501 taagatctac tatgtctatg gcttcatgat gctgggtgctg gtcacccctgt gcattgtgac
1561 tgtctgtgtg accattgtct gcacatactt cctgctaaac gcagaggatt acagggtggca
1621 gtggacgagt ttctgtctg cggcgtcgac cggatctac gtttacctgt actcctttta
1681 ctactacttc ttcaaaacca agatgtatgg cttatttcaa acatcatttt actttggcta
1741 catggcggtg tttagcacag ccttggggat aatgtgtgga gcaatcggtt acatgggaac
1801 aagtgccttt gtgcgaaaaa tctatactaa tgtgaaaatt gactagatat ctgagacaac
1861 atggaaacttc ggatcagttt ctctttcatg aggggtggaac ttgcacagaa aagaagaata
1921 atcgcaagaa gagatttggg cttaacactg ggtactttgt gggctctctt tgggatggc
1981 ttcaagtaac atctatttcc attgatccta ggttcttact gactgctttc tccagctgtt
2041 cacagcagat gcttggattt tatgcagtag gctttactac agtacatggc taatcttccc
2101 caaactagct cattaaagat gaaatagacc agctctcttc agtgaagagg acaaatagtt
2161 tatttaaagc atttgttcca ataaaataac tagagggaac cttggatgct aaaattccat
2221 aagtagaaaa atcttcctgg cacttgggtt ttctatgtta ttgaaaaatg atgttccaga
2281 aagattactt ttctttttat ttttactgcc attgttgatg tgttgggga catttttata
2341 tattgaacct gggttctttt ttgatctgtt ttggtcgtcc ctccattcaa ctgcatcttt
2401 tttttttttt aaaaacaaaa ttaaaagcta ttcaattctg catggaatat atctgctgtc
2461 atcttaatct tagtttggat caacctcatt tatttatctt aaaattaacc agctttctca
2521 gttccatcca aagaagatac agtatgaaag tagaggtgca ctctctataa tacaatctac
2581 tgtacagtta gcaagcgaag tgttaaatgg agaagatgct tgtttttatt aaacatttgg
2641 agatttagat aattttacatt ttaactgaat gtctaaagtg attatcttcc cctccctccc
2701 ccaagttaat ctccatctt tgtttttggg ttcaaatgaa ggctttacat aagaaattat
2761 taaacaaaaa aaggggggca ataatgtat ataacattaa taatgtcgcg taggtgtagg
2821 ttctgggatg catttggatg tacagactga ctgggggact gtattgcgat gatgattggt
2881 gtagaaacgt atgggtctgg gtggcctttt acatcttgcc taccattgca tgaacattg
2941 gggtttcttc aaaatgtgtg tgcatactt cttttgggag ggggttgtt tcttcttta
3001 tgaactcct actggagctc aatttgaat ttagaaacat ttaattttgt taatcctgtc
3061 tgggacattt aggtaacatc taaagcatta ttgottttaga atgttcaaat aaaatttcct
3121 gaccaaaaaa aaaaaaaaaa aaa

//

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

May 20 2003 11:20:12



Search for

Display Show:

Links

1: AY071401. Drosophila melano...[gi:17945956]

LOCUS AY071401 2662 bp mRNA linear INV 20-DEC-2001
DEFINITION Drosophila melanogaster RE48767 full length cDNA.
ACCESSION AY071401
VERSION AY071401.1 GI:17945956
KEYWORDS FLI_CDNA.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 2662)
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M.
and Celniker, S.

TITLE Direct Submission
JOURNAL Submitted (18-DEC-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA

COMMENT Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(<http://fruitfly.berkeley.edu>) or send email to
cdna@fruitfly.berkeley.edu.

FEATURES
source 1..2662
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
/map="64E3-64E3"
gene 1..2662
/gene="CG10590"
/note="alignment with genomic scaffold AE003565"
/db_xref="FLYBASE:FBgn0035622"
CDS 178..1956
/gene="CG10590"
/note="Longest ORF"
/codon_start=1
/product="RE48767p"
/protein_id="AAL49023.1"
/db_xref="GI:17945957"
/db_xref="FLYBASE:FBgn0035622"
/translation="MGSSATOTTVPFRAICLCLL IASCVVLSQADEHNHXYNDREEV
VLWMNTVGPYHNROETAYFSLPFCSGQKSSI SHYHETLSEALQGVLEFGYEMEFK
SDAPKSVICMVTLOEESAKAFTYAVKNEYWQYIDGLPIWGVGERDERDGKYYIFT
HKKFDIGYNGQQIVDITLTTEGREELKPGSHINFSYEVNWKPSKVEFKNRFDKYLDPN
FFQHR IHWFSI FNSFMVIFLVGLVSNILMRTLKDYARYSKDEEIDDMERDLGDEYG
WKQVHGDVFRSPNTLLFSALVGAGYQLISVVFCVIMFAIVGELYTERGSMLSTAFV
YAATSPINGYFGGSLYARLGGRMWIRQMLVSAFTVPVAVCGTAFINFIAGYHASRA
IPFGTMVAVTCICLFVILPLTLVGTVVRNLDGQPDFCRVNAVPRPIPEKKWYMEPL
IIVLLGGVLPFGSIFIMYFIFTSFWAYKIYYVYGFMLLVFSILTVTVCVTVICVTF
LLNAEDYRWQWTSFMAAGSTSIYVYAYSFYFFFKTKMFGLFOTAFYFGYMA LFSGAL
GICGTGVGYVGTNLFRKIYSNVKID"

BASE COUNT 672 a 651 c 613 g 726 t


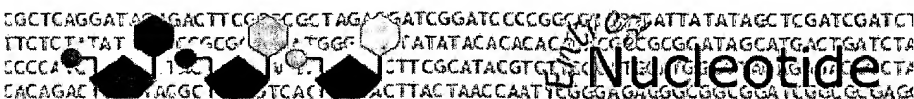
ORIGIN

```
1 atcgaatgtt ctccacctt aagatacaac cctaaaaatat ttctgtgtc ggcaaatctg
61 agtgtttgcc acaaaactgt ttgaaaacgc aatcccagcg agggcaaccg aatcaggccg
121 gcagagcgag gtcaccagga agacgcgcaa acgaggtcac cacctgcaca agacacaatg
181 ggagagcgag ccacgcaaac cacggtgccg ttccgtgcaa ttgtttatg tctgtgatc
241 gccagctgct acgtgtcgct ctcccaggca gatgagcaca atcacaagta caatgaccgg
301 gaggaggtgg tactgtggat gaacacggtg ggcccgtacc acaatcggca ggagacgtac
361 gcgtacttct ctctcccttt ttgcagtggc cagaagtcct cgatatcgca ctaccacgag
421 acgtgagcgc aggcgtgca aggagtcgag cttaggttca gtggctacga gatggagttc
481 aagagcgacg ccccaaatc ggatcatctg atggtcacct tgcaggagga gagcgccaag
541 gcattcacct atgcccgtga gaacgagtag tggtagcaga tgtacatcga tggactgcc
601 atttggggaa aagtgggtga gcgcgacgag cgcgatggca agtactatat cttcacgcac
661 aagaagtctg acatcggcta caatggccag caaatcgtgg atatcacctt gaccaccgag
721 ggccgagagg aactcaagcc gggatccac atcaacttct cctacgaggt caactggaag
781 cccagcaagg tggagtccaa gaatcgattc gacaagtacc tggatcccaa cttcttccag
841 cacaggatcc actgggttcag catcttcaac agcttcatga tggatcatct cctgggtggg
901 ctggtgtcca tgattctgat gcgaactctg cgcgaaggat atgtcggta cagtaaggac
961 gaggaaatcg acgacatgga gcgagatctt ggtgatgaat acggctggaa gcagggtgat
1021 ggagatgtct tccgttctcc gcccaacaca ctgctcttct cggcgttggg ggccgctgga
1081 tacaacttga ttccgttgtt attctgtgtg atcatgttcg ccatagttag tgaattgtac
1141 acggaacgag gctccgttga gtccacggct atatttgtt atgccgcac ctcaccaatc
1201 aatggatact ttggaggatc gctctatgcc cgcctgggtg gacgcatgtg gatccgacag
1261 atgctgtgtt ccgcttttcc agttccagtg gctgtgtgcg gcacggcttt cctgatcaac
1321 ttcattgcca ttggatatca cgcgtcgaga gccattccct toggatccat ggtggcggtc
1381 acttgcatct cctgttttgg catcctgccc ttgactctgg tgggtactgt cgtggccgc
1441 aatcggagc gcccaaccaga ctttccatgc cgcgtcaacg cgggtccacg accattccc
1501 gaaaagaagt ggtacatgga gccactgatt attgtgcttc ttggcgggtg cttgcccttt
1561 ggatccatct tcattgagat gtacttcac ttcaactcct tctggcgta caagatctac
1621 tacgtctacg gcttcatgtt gctgttttc agcatcctga ctgtgtcac cgtgtgctc
1681 accatcgtgt gcacctactt cctgctaaat gccgaagatt accgatggca gtggacgagt
1741 ttcattgctg cgggctccac gtcgatttac gtgtacgctt atctcttcta ttacttctc
1801 tttaaaacca aaatgttccg tctgttccaa acggccttct actttggcta catggcactc
1861 ttcagcggcg ccttgggcat tatctgggc accgtcggct atgtgggcac gaatctctc
1921 gtgcgcaaaa tctattccaa tgtgaaaata gactaagagc cctgcgactg caaaccacc
1981 ccagatctg tatatcatcc taatcgatta acaattgtat ttattgagta gatttttagt
2041 tctgtttcac aacttttagt ccagtgggt ctccctttt cgtctctttg ggttaccac
2101 ttctcatgtt ggtgtgaaaa tgaatgccag tccaatatat tgcacacaaa gataaaagat
2161 tcagtttaac gatgtatag caaactacat atatcaccta aaaggtttac ttcggaatta
2221 taagactaga cgtttcaaat gagaaaattt gggaaaacat tgtgaattaa aagctctttc
2281 tgttgcattt acgttttctt agttttaaga gtcaattaat cctatacact aatttttgg
2341 tttgtaattt ctactgttcc ataaaataac atttctctac ttacttaaat tactaagaag
2401 cttgcttaca caaaatattt gatataattt cgaagataac ttttatgtca tatatgtcg
2461 tatgttactg tgcatacggg gtacatcgag tattttattt gaattgttg cctagaaaac
2521 ttatcaatct atgcaactgc aacaaaatgt gacttgaact tgtttgcgcc aattaagtta
2581 tgtacgatgc aagaaatgtg ctgattagca atagtcgata atctaataat aaattcaata
2641 tataaaacca aaaaaaaaaa aa
```

//

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

May 20 2003 11:20:17

  Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Display Show: Send to

☐ 1: Z28655. HSB72F051 STRATAG...[gi:434270]

[Links](#)

IDENTIFIERS

dbEST Id: 38740
EST name: HSB72F051
GenBank Acc: Z28655
GenBank gi: 434270

CLONE INFO

Clone Id: 72F05
DNA type: cDNA

PRIMERS

PolyA Tail: Unknown

SEQUENCE

```
CAGATGTCATATTTCAGTAAAATGGAAAAAGTCAGATGTGAAATTTGANGATCGATTTGAC
AAATATCTTGATCCGTCCTTTTTTCAACATCGGATTCATTGGTTTTCAATTTTCAACTCC
TTCATGATGGTGATCTTCTTGGTGGGCTTAGTTTCAATGATTTTAATGAGAACATTAAGA
AAAGATTATGCTCGGTACAGTAAAGAGGAAGAAATGGATCATATCGATAGAGACCTAGGA
GATGAATATGGATGGAACAGGTGCATGGAGATGTATTTAGACCATCAAGTCACCCA
```

Entry Created: Dec 14 1993
Last Updated: Dec 14 1993

COMMENTS

strand(-), single read

LIBRARY

Lib Name: STRATAGENE Human skeletal muscle cDNA library, cat. #936215.
Organism: Homo sapiens
Sex: Female
Organ: leg muscle
Tissue type: skeletal muscle
Develop. stage: 19 years
Vector: Lambda ZAPII
Description: Tissue from female, 19 years old, normal leg muscle. Cloning vector is Lambda ZAPII, in vivo excision from lambda ZAPII to pBluescript SK(+). Genexpress library reference is B.

SUBMITTER

Name: Genethon
Lab: Genexpress-Genethon
Institution: Genethon Centre de recherche sur le Genome Humain
Address: 1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
E-mail: genexpress@genethon.fr

CITATIONS

Medline UID: [95277534](#)

Title: IMAGE: molecular integration of the analysis of the human genome and its expression
Authors: Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C., Tessier,A.
Citation: C. R. Acad. Sci. III, Sci. Vie 318 (2): 263-272 1995

MAP DATA

Revised: July 5, 2002.

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Mar 6 2003 11:00:01